ALK-5

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 04:11:00 1997; MasPar time 1905.03 Seconds
1347.129 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GGCGAGGCGAGGTTTGCTGG.....TGTTAAAACCTATAGTGTTT 2308
Comp: CCGCTCCGCTCCAAACGACC.....ACAATTTTGGATATCACAAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-new11
1:BCT 2:FUN 3:GEN 4:HUM5 5:HUM2 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2

Database: genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9

Database: genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:UNA 114:VRL

Database: u-embl48_97
115:part1 116:part2

Statistics: Mean 12.312; Variance 5.693; scale 2.089

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2308	100.0	2308	75	HUMALK5A	Human activin recepto	0.00e+00
2	1253	54.3	2860	86	MUSTGFB1R	Mouse mRNA for TGF-be	0.00e+00
3	1221	52.9	1381	47	MSU37065	Mustela sp. TGF-b typ	0.00e+00
4	1150	49.8	1659	20	MMTGFBTI	Mouse mRNA for TGF-be	0.00e+00
5	1150	49.8	1659	86	MUSTGFBIR	Mouse mRNA for TGF-be	0.00e+00
6	1102	47.7	1506	55	I23851	Sequence 4 from paten	0.00e+00
7	1102	47.7	1506	55	I25010	Sequence 4 from paten	0.00e+00
8	1102	47.7	1545	87	RATSETHKIR	Rat transforming grow	0.00e+00
9	833	36.1	2186	49	CHKRPK2	Chicken RPK-2 mRNA fo	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS HUMALK5A 2308 bp mRNA PRI 24-JAN-1994
DEFINITION Human activin receptor-like kinase (ALK-5) mRNA, complete cds.
ACCESSION L11695
NID g431034
KEYWORDS activin; activin receptor-like kinase; serine/threonine kinase; transforming growth factor-beta; transmembrane protein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2308)
AUTHORS Franzen,P., ten Dijke,P., Ichijo,H., Yamashita,H., Schulz,P., Heldin,C.H. and Miyazono,K.
TITLE Cloning of a TGF beta type I receptor that forms a heteromeric complex with the TGF beta type II receptor
JOURNAL Cell 75 (4), 681-692 (19[illegible])
MEDLINE 94061986

Query Match 100.0%; Score 2308; DB 75; Length 2308;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 2308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
LOCUS MUSTGFB1R 2860 bp mRNA ROD 04-OCT-1994
DEFINITION Mouse mRNA for TGF-beta type I receptor, complete cds.
ACCESSION D25540
NID g483375
KEYWORDS TGF-beta type I receptor; serine/threonine kinase receptor; transforming growth factor-beta type I receptor.
SOURCE Mus musculus brain cDNA to mRNA.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2860)
AUTHORS Suzuki,A., Shioda,N., Maeda,T., Tada,M. and Ueno,N.
TITLE A mouse TGF-beta type I receptor that requires type II receptor for ligand binding
JOURNAL Biochem. Biophys. Res. Commun. 198 (3), 1063-1069 (1994)
MEDLINE 94161715

Query Match 54.3%; Score 1253; DB 86; Length 2860;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1537; Conservative 0; Mismatches 170; Indels 19; Gaps 11;

RESULT 3
LOCUS MSU37065 1381 bp mRNA MAM 31-OCT-1995
DEFINITION Mustela sp. TGF-b type I receptor mRNA, partial cds.
ACCESSION U37065
NID g1045609
KEYWORDS .
SOURCE mink.
ORGANISM Mustela sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustela.
REFERENCE 1 (bases 1 to 1381)
AUTHORS Weis-Garcia,F. and Massague,J.
TITLE Complementation between kinase-defective and activation-defective TGF-b receptors reveals a novel form of receptor cooperativity
JOURNAL EMBO J. (1995) In press
REFERENCE 2 (bases 1 to 1381)
AUTHORS Weis-Garcia,F.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1995) Frances Weis-Garcia, Cell Biology &

RESULT 4
ID MMTGFBTI standard; RNA; ROD; 1659 BP.
AC D28526;
NI g467521

DT 26-FEB-1994 (Rel. 38, Created)
DT 08-SEP-1996 (Rel. 49, Last updated, Version 4)
DE Mouse mRNA for TGF-beta type I receptor, complete cds.
KW TGF-beta type I receptor.
OS Mus musculus (mouse)
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
RN [1]
RP 1-1659
RA Tomoda T.;
RT ;
RL Submitted (26-JAN-1994) to the EMBL/GenBank/DDBJ databases.
RL Toshifumi Tomoda, Institute of Medical Science, The University of
RL Tokyo, Molecular and Developmental Biology; 4-6-1 Shirokanedai,
RL Minato-ku, Tokyo 108, Japan (E-mail:ynakagaw@ims.u-tokyo.ac.jp,
RL Tel:03-3443-8111(ex.660), Fax:03-3443-5320)
RN [2]
RP 1-1659
RX MEDLINE; 94161714.
RA Tomoda T., Kudoh T., Noma T., Nakazawa A., Muramatsu M., Arai K.;
RT "Molecular cloning of a mouse counterpart for human TGF-beta type
RT I receptor";
RL Biochem. Biophys. Res. Commun. 198:1054-1062(1994).
CC Submitted (26-Jan-1994) to DDBJ by: Toshifumi Tomoda Molecular and
CC Developmental Biology Institute of Medical Science The University
CC of Tokyo 4-6-1 Shirokanedai Minato-ku Tokyo 108 Japan Phone:
CC 03-3443-8111 Fax: 03-3443-5320.

Query Match 49.8%; Score 1150; DB 20; Length 1659;
Best Local Similarity 89.2%; Pred. No. 0.00e+00;
Matches 1445; Conservative 0; Mismatches 151; Indels 24; Gaps 8;

RESULT 6
LOCUS I23851 1506 bp DNA PAT 26-JUL-1996
DEFINITION Sequence 4 from patent US 5538892.
ACCESSION I23851
NID g1603721
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1506)
AUTHORS Donahoe,P.K., Gustafson,M., He,W. and Wang,X.
TITLE Nucleic acids encoding a TGF-.beta. type 1 receptor
JOURNAL Patent: US 5538892-A 4 23-JUL-1996;

FEATURES Location/Qualifiers
source 1..1506
/organism="unknown"
BASE COUNT 428 a 321 c 363 g 394 t
ORIGIN

Query Match 47.7%; Score 1102; DB 55; Length 1506;
Best Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;

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Db     51 ggtggcggcggcgacgctgctcccgggggcgaaggcattacagtgtttctgccacctctg 110
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Qy    139 GGCGGCGGCGGCGGCGCTGCTCCCGGGGGCGACGGCGTTACAGTGTTTCTGCCACCTCTG 198

Db    111 tacaaaggacaattttacttgtgagacagatggtctctgctttgtctcagtcaccgagac 170
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Qy    199 TACAAAAGACAATTTTACTTGTGTGACAGATGGGCTCTGCTTTGTCTCTGTCACAGAGAC 258

Db    171 cacagacaaagttatacacaatagcatgtgtatagctgaaatcgacctaattccccgaga 230
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Qy    259 CACAGACAAAGTTATACACAACAGCATGTGTATAGCTGAAATTGACTTAATTCCTCGAGA 318

Db    231 caggccatttgtttgtgcaccatcttcaaaaacaggggcagttacgtattgctgcaatca 290
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Qy    319 TAGGCCGTTTGTATGTGCACCCTCTTCAAAAACTGGGTCTGTGAC-TACAACAT--ATT- 374

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Qy    375 GCTGCAAT-CAGGACCATTGCAATAAAATAGA-ACTTCCAACTACTGTAAAGTCATCACC 432

Db    351 tggcctcggtcctgtggagctggcagctgtcattgctggtccagtctgcttcgtctgcat 410
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Qy    433 TGGCCTTGGTCCTGTGGAACTGGCAGCTGTCATTGCTGGACCAGTGTGCTTCGTCTGCAT 492

Db    411 tgcacttatgctgatggtctatatctgccataaccgcactgtcattcaccaccgcgtgcc 470
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Qy    493 CTCACTCATGTTGATGGTCTATATCTGCCACAACCGCACTGTCATTCACCATCGAGTGCC 552

Db    471 aaatgaagaggatccctcactagatcgccctttcatttcagagggcaccaccttaaaaga 530
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Qy    553 AAATGAAGAGGACCCTTCATTAGATCGCCCTTTTATTTCAGAGGGTACTACGTTGAAAGA 612

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Qy    673 AACAATTGCGAGAACTATTGTGTTACAAGAAAGCATTGGCAAAGGTCGATTTGGAGAAGT 732

Db    651 ttggcgaggcaaatggcggggagaagaagttgccgtgaagatattctcttctagagaaga 710
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Qy    733 TTGGAGAGGAAAGTGGCGGGGAGAAGAAGTTGCTGTTAAGATATTCTCCTCTAGAGAAGA 792

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Qy    793 ACGTTCGTGGTTCCGTGAGGCAGAAAATATCAAACTGTAATGTTACGTCATGAAAACAT 852

Db    771 cctggggtttatagcagcagacaacaaagacaatggtacatggactcagctgtggttggt 830
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Qy    853 CCTGGGATTTATAGCAGCAGACAATAAAGACAATGGTACTTGGACTCAGCTCTGGTTGGT 912

Db    831 gtcggattatcatgagcatggatccctttttcgattacttgaatagatacactgttactgt 890
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Qy    913 GTCAGATTATCATGAGCATGGATCCCTTTTTGATTACTTAAACAGATACACAGTTACTGT 972

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Qy    973 GGAAGGAATGATAAAACTTGCTCTGTCCACGGCGAGCGGTCTTGCCCATCTTCACATGGA 1032

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Qy   1033 GATTGTTGGTACCCAAGGAAAGCCAGCCATTGCTCATAGAGATTTGAAATCAAAGAATAT 1092

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Qy   1093 CTTGGTAAAGAAGAATGGAACTTGCTGTATTGCAGACTTAGGACTGGCAGTAAGACATGA 1152

Db   1071 ttctgccacagatacaattgatattgctccaaaccacagagtaggcactaaaaggtatat 1130
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Qy   1153 TTCAGCCACAGATACCATTGATATTGCTCCAAACCACAGAGTGGGAACAAAAAGGTACAT 1212

Db   1131 ggccccctgaagttctagatgattccataaatatgaaacattttgaatccttcaaacgtgc 1190
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Qy   1213 GGCCCCTGAAGTTCTCGATGATTCCATAAATATGAAACATTTTGAATCCTTCAAACGTGC 1272

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Qy   1273 TGACATCTATGCAATGGGCTTAGTATTCTGGGAAATTGCTCGACGATGTTCCATTGGTGG 1332

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Qy   1333 AATTCATGAAGATTACCAACTGCCTTATTATGATCTTGTACCTTCTGACCCATCAGTTGA 1392

Db   1311 agaaatgagaaaagtagtttgtgaacagaagttaaggccaaatattcccaacagatggca 1370
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Db   1371 gagctgtgaggccttgagagtgatggccaaaattatgagagaatgttggtatgccaatgg 1430
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Qy   1453 GAGCTGTGAAGCCTTGAGAGTAATGGCTAAAATTATGAGAGAATGTTGGTATGCCAATGG 1512

Db   1431 agcagctaggctgacagctttgcgaattaaaaaaacattgtcacagctcagccaacagga 1490
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Qy   1513 AGCAGCTAGGCTTACAGCATTGCGGATTAAGAAAACATTATCGCAACTCAGTCAACAGGA 1572

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Qy   1573 AGGCATCAAAATGTAA 1588


RESULT    7
LOCUS       I25010       1506 bp    DNA             PAT       21-AUG-1996
DEFINITION  Sequence 4 from patent US 5547854.
ACCESSION   I25010
NID         g1604880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1506)
  AUTHORS   Donahoe,P.K., Gustafson,M. and He,W.W.
  TITLE     DNA encoding a receptor for Mullerian inhibitory substance, misr1,
            and corresponding vectors, cells, probes, and recombinant methods
  JOURNAL   Patent: US 5547854-A 4 20-AUG-1996;

FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      428 a    321 c    363 g    394 t
ORIGIN

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  Best Local Similarity  88.9%;  Pred. No. 0.00e+00;
  Matches  1294;  Conservative    0;  Mismatches  156;  Indels   6;  Gaps   5;

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Qy    139 GGCGGCGGCGGCGGCGCTGCTCCCGGGGGCGACGGCGTTACAGTGTTTCTGCCACCTCTG 198

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Qy    199 TACAAAAGACAATTTTACTTGTGTGACAGATGGGCTCTGCTTTGTCTCTGTCACAGAGAC 258

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Qy    319 TAGGCCGTTTGTATGTGCACCCTCTTCAAAAACTGGGTCTGTGAC-TACAACAT--ATT- 374

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Qy    375 GCTGCAAT-CAGGACCATTGCAATAAAATAGA-ACTTCCAACTACTGTAAAGTCATCACC 432

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Qy    433 TGGCCTTGGTCCTGTGGAACTGGCAGCTGTCATTGCTGGACCAGTGTGCTTCGTCTGCAT 492

Db    411 tgcacttatgctgatggtctatatctgccataaccgcactgtcattcaccaccgcgtgcc 470
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Qy    493 CTCACTCATGTTGATGGTCTATATCTGCCACAACCGCACTGTCATTCACCATCGAGTGCC 552

Db    471 aaatgaagaggatccctcactagatcgccctttcatttcagagggcaccaccttaaaaga 530
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Qy    553 AAATGAAGAGGACCCTTCATTAGATCGCCCTTTTATTTCAGAGGGTACTACGTTGAAAGA 612

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Qy    613 CTTAATTTATGATATGACAACGTCAGGTTCTGGCTCAGGTTTACCATTGCTTGTTCAGAG 672

Db    591 aacaattgcaaggaccattgtgctacaagaaagcatcggcaaaggtcggtttggagaagt 650
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Qy    673 AACAATTGCGAGAACTATTGTGTTACAAGAAAGCATTGGCAAAGGTCGATTTGGAGAAGT 732

Db    651 ttggcgaggcaaatggcggggagaagaagttgccgtgaagatattctcttctagagaaga 710
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Qy    733 TTGGAGAGGAAAGTGGCGGGGAGAAGAAGTTGCTGTTAAGATATTCTCCTCTAGAGAAGA 792

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Qy    793 ACGTTCGTGGTTCCGTGAGGCAGAGATTTATCAAACTGTAATGTTACGTCATGAAAACAT 852

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Qy    853 CCTGGGATTTATAGCAGCAGACAATAAAGACAATGGTACTTGGACTCAGCTCTGGTTGGT 912

Db    831 gtcggattatcatgagcatggatccctttttcgattacttgaatagatacactgttactgt 890
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Qy    913 GTCAGATTATCATGAGCATGGATCCCTTTTTGATTACTTAAACAGATACACAGTTACTGT 972

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Qy    973 GGAAGGAATGATAAAACTTGCTCTGTCCACGGCGAGCGGTCTTGCCCATCTTCACATGGA 1032

Db    951 gattgttggtacccaaggaaaaccagctattgcccatagagatttgaaatcaaagaatat 1010
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Qy   1093 CTTGGTAAAGAAGAATGGAACTTGCTGTATTGCAGACTTAGGACTGGCAGTAAGACATGA 1152

Db   1071 ttctgccacagatacaattgatattgctccaaaccacagagtaggcactaaaaggtatat 1130
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Qy   1153 TTCAGCCACAGATACCATTGATATTGCTCCAAACCACAGAGTGGGAACAAAAAGGTACAT 1212

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Qy   1273 TGACATCTATGCAATGGGCTTAGTATTCTGGGAAATTGCTCGACGATGTTCCATTGGTGG 1332

Db   1251 aatccacgaagactaccagttgccttactatgatcttgtaccttctgatccatccgttga 1310
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Qy   1333 AATTCATGAAGATTACCAACTGCCTTATTATGATCTTGTACCTTCTGACCCATCAGTTGA 1392

Db   1311 agaaatgagaaaagtagtttgtgaacagaagttaaggccaaatattcccaacagatggca 1370
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Qy   1393 AGAAATGAGAAAAGTTGTTTGTGAACAGAAGTTAAGGCCAAATATCCCAAACAGATGGCA 1452

Db   1371 gagctgtgaggccttgagagtgatggccaaaattatgagagaatgttggtatgccaatgg 1430
          ||||||||| |||||||||| ||||| ||||||||||||||||||||||||||||||||
Qy   1453 GAGCTGTGAAGCCTTGAGAGTAATGGCTAAAATTATGAGAGAATGTTGGTATGCCAATGG 1512

Db   1431 agcagctaggctgacagctttgcgaattaaaaaaacattgtcacagctcagccaacagga 1490
          |||||||||||| ||||| ||||| ||||| |||||||| || || ||||| ||||||||
Qy   1513 AGCAGCTAGGCTTACAGCATTGCGGATTAAGAAAACATTATCGCAACTCAGTCAACAGGA 1572

Db   1491 aggcatcaaaatgtaa 1506
          ||||||||||||||||
Qy   1573 AGGCATCAAAATGTAA 1588


RESULT    8
LOCUS       RATSETHKIR   1545 bp    mRNA            ROD       11-DEC-1995
DEFINITION  Rat transforming growth factor beta type I receptor mRNA, complete
```

```
            cds.
ACCESSION   L26110
NID         g416397
KEYWORDS    serine/threonine kinase receptor.
SOURCE      Rattus norvegicus (strain Sprague-Dawley) cDNA to mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Rattus.
REFERENCE   1  (bases 1 to 1545)
  AUTHORS   He,W.W., Gustafson,M.L., Hirobe,S. and Donahoe,P.K.
  TITLE     Developmental expression of four novel serine/threonine kinase
            receptors homologous to the activin/transforming growth factor-beta
            type II receptor family
  JOURNAL   Dev. Dyn. 196 (2), 133-142 (1993)
  MEDLINE   93372378
REFERENCE   2  (bases 1 to 1545)
  AUTHORS   Bassing,C.H., Yingling,J.M., Howe,D.J., Wang,T., He,W.W.,
            Gustafson,M.L., Shah,P., Donahoe,P.K. and Wang,X.F.
  TITLE     A transforming growth factor beta type I receptor that signals to
            activate gene expression
  JOURNAL   Science 263 (5143), 87-89 (1994)
  MEDLINE   94098329
FEATURES             Location/Qualifiers
     source          1..1545
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /dev_stage="14.5-15 day fetus"
                     /tissue_type="urogenital ridge"
                     /clone="R4"
     CDS             40..1545
                     /note="serine/threonine kinase receptor; TGF-beta type I"
                     /codon_start=1
                     /product="transforming growth factor beta type I receptor"
                     /db_xref="PID:g1113130"
                     /translation="MEAASAALRRCLLLIVLVAAATLLPGAKALQCFCHLCTKDNFTC
                     ETDGLCFVSVTETTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGAVTYCCNQDHCNK
                     IELPTTGPFSEKQSAGLGPVELAAVIAGPVCFVCIALMLMVYICHNRTVIHHRVPNEE
                     DPSLDRPFISEGTTLKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVW
                     RGKWRGEEVAVKIFSSREERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWL
                     VSDYHEHGSLFDYLNRYTVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKS
                     KNILVKKNGTCCIADLGLAVRHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFE
                     SFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRP
                     NIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQEGIKM"
BASE COUNT      435 a    335 c    380 g    395 t
ORIGIN
```

```
Query Match           47.7%;  Score 1102;  DB 87;  Length 1545;
Best Local Similarity  88.9%;  Pred. No. 0.00e+00;
Matches  1294;  Conservative    0;  Mismatches 156;  Indels   6;  Gaps   5;

Db     90 ggtggcggcggcgacgctgctcccgggggcgaaggcattacagtgtttctgccacctctg 149
          || |||||||||| |||||||||||||||||||| ||| |||||||||||||||||||||||
Qy    139 GGCGGCGGCGGCGGCGCTGCTCCCGGGGGCGACGGCGTTACAGTGTTTCTGCCACCTCTG 198

Db    150 tacaaaggacaatttttacttgtgagacagatggtctctgctttgtctcagtcaccgagac 209
          |||||| |||||||||||||||| ||||||||| |||||||||||||| ||||| |||||
Qy    199 TACAAAAGACAATTTTACTTGTGTGACAGATGGGCTCTGCTTTGTCTCTGTCACAGAGAC 258

Db    210 cacagacaaagttatacacaatagcatgtgtatagctgaaatcgacctaattccccgaga 269
          |||||||||||||||||||||||||||||||||||||||||||| ||| |||||||| |||||
Qy    259 CACAGACAAAGTTATACACAACAGCATGTGTATAGCTGAAATTGACTTAATTCCTCGAGA 318

Db    270 caggccatttgtttgtgcaccatcttcaaaaacaggggcagttacgtattgctgcaatca 329
          |||||  |||||  |||||||| |||||||||||| ||| | || || ||   |    ||
Qy    319 TAGGCCGTTTGTATGTGCACCCTCTTCAAAAACTGGGTCTGTGAC-TACAACAT--ATT- 374

Db    330 ggatcactgcaataaaatagaactcccaactacaggacctttttcagaaaagcagtcagc 389
          |   || | ||  |  || | | |   |  | |   ||   | | | ||||   ||| |
Qy    375 GCTGCAAT-CAGGACCATTGCAATAAAATAGA-ACTTCCAACTACTGTAAAGTCATCACC 432

Db    390 tggcctcggtcctgtggagctggcagctgtcattgctggtccagtctgcttcgtctgcat 449
          |||||| |||||||||| |||||||||||||||||||| ||||| ||||||||||||||
Qy    433 TGGCCTTGGTCCTGTGGAACTGGCAGCTGTCATTGCTGGACCAGTGTGCTTCGTCTGCAT 492

Db    450 tgcacttatgctgatggtctatatctgccataaccgcactgtcattcaccaccgcgtgcc 509
          |||| ||| |||||||||||||||||||| |||||||||||||||||||| || |||||
Qy    493 CTCACTCATGTTGATGGTCTATATCTGCCACAACCGCACTGTCATTCACCATCGAGTGCC 552

Db    510 aaatgaagaggatccctcactagatcgccctttcatttcagagggcaccaccttaaaaga 569
          |||||||||||| || ||| |||||||||||||| |||||||||| || || || |||||
Qy    553 AAATGAAGAGGACCCTTCATTAGATCGCCCTTTTATTTCAGAGGGTACTACGTTGAAAGA 612

Db    570 tttaatttatgatatgacaacatcagggtctggatcaggtttaccactgcttgttcaaag 629
          |||||||||||||||||||| ||||| ||||| |||||||||||| |||||||||| ||
Qy    613 CTTAATTTATGATATGACAACGTCAGGTTCTGGCTCAGGTTTACCATTGCTTGTTCAGAG 672

Db    630 aacaattgcaaggaccattgtgctacaagaaagcatcggcaaaggtcggtttggagaagt 689
          ||||||||| || || |||||| |||||||||||| |||||||||| ||||||||||
Qy    673 AACAATTGCGAGAACTATTGTGTTACAAGAAAGCATTGGCAAAGGTCGATTTGGAGAAGT 732

Db    690 ttggcgaggcaaatggcggggagaagaagttgccgtgaagatattctcttctagagaaga 749
          |||| |||| || |||||||||||||||||||| || |||||||||| ||||||||||
Qy    733 TTGGAGAGGAAAGTGGCGGGGAGAAGAAGTTGCTGTTAAGATATTCTCCTCTAGAGAAGA 792

Db    750 acgttcatggttccgagaggcagagatttatcagactgtaatgttacgccatgaaaatat 809
          |||||| |||||||| |||||||||||||| |||||||||||||| |||||||| ||
Qy    793 ACGTTCGTGGTTCCGTGAGGCAGAGATTTATCAAACTGTAATGTTACGTCATGAAAACAT 852

Db    810 cctggggtttatagcagcagacaacaaagacaatggtacatggactcagctgtggttggt 869
          |||||| |||||||||||||||||||||||||||||||||| |||||||||| ||||||
Qy    853 CCTGGGATTTATAGCAGCAGACAATAAAGACAATGGTACTTGGACTCAGCTCTGGTTGGT 912

Db    870 gtcggattatcatgagcatggatccctttttcgattacttgaatagatacactgttactgt 929
          ||| |||||||||||||||||||||||||||| |||||||| || |||||||| ||||||||
Qy    913 GTCAGATTATCATGAGCATGGATCCCTTTTTGATTACTTAAACAGATACACAGTTACTGT 972

Db    930 ggaaggaatgatcaaactcgctctgtccacggcaagtggtcttgcccatcttcacatgga 989
          |||||||||||| ||||| |||||||||||||| || ||||||||||||||||||||||
Qy    973 GGAAGGAATGATAAAACTTGCTCTGTCCACGGCGAGCGGTCTTGCCCATCTTCACATGGA 1032

Db    990 gattgttggtacccaaggaaaaccagctattgcccatagagatttgaaatcaaagaatat 1049
          |||||||||||||||||||| ||||| ||||| ||||||||||||||||||||||||||
Qy   1033 GATTGTTGGTACCCAAGGAAAGCCAGCCATTGCTCATAGAGATTTGAAATCAAAGAATAT 1092

Db   1050 cttggtgaagaaaaatggaacctgttgtattgcagatttgggacttgctgtgagacatga 1109
          |||||| ||||| |||||||| || |||||||||| || ||||| || || ||||||||
Qy   1093 CTTGGTAAAGAAGAATGGAACTTGCTGTATTGCAGACTTAGGACTGGCAGTAAGACATGA 1152

Db   1110 ttctgccacagatacaattgatattgctccaaaccacagagtaggcactaaaaggtatat 1169
          ||| |||||||||| |||||||||||||||||||||||||| || || |||||||| ||
Qy   1153 TTCAGCCACAGATACCATTGATATTGCTCCAAACCACAGAGTGGGAACAAAAAGGTACAT 1212

Db   1170 ggcccctgaagttctagatgattccataaatatgaaacattttgaatccttcaaacgtgc 1229
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy   1213 GGCCCCTGAAGTTCTCGATGATTCCATAAATATGAAACATTTTGAATCCTTCAAACGTGC 1272

Db   1230 tgacatctatgcaatgggcttagtattctgggaaatcgctcgacgctgttccattggcgg 1289
          |||||||||||||||||||||||||||||||||||||||||| |||||||| |||||||| ||
Qy   1273 TGACATCTATGCAATGGGCTTAGTATTCTGGGAAATTGCTCGACGATGTTCCATTGGTGG 1332

Db   1290 aatccacgaagactaccagttgccttactatgatcttgtaccttctgatccatccgttga 1349
          ||| || ||||| |||||  ||||||| |||||||||||||||||||| ||||| |||||
Qy   1333 AATTCATGAAGATTACCAACTGCCTTATTATGATCTTGTACCTTCTGACCCATCAGTTGA 1392

Db   1350 agaaatgagaaaagtagtttgtgaacagaagttaaggccaaatattcccaacagatggca 1409
          |||||||||||||| |||||||||||||||||||||||||||||||| || ||||||||||
Qy   1393 AGAAATGAGAAAAGTTGTTTGTGAACAGAAGTTAAGGCCAAATATCCCAAACAGATGGCA 1452

Db   1410 gagctgtgaggccttgagagtgatggccaaaattatgagagaatgttggtatgccaatgg 1469
          ||||||||| |||||||||| ||||| |||||||||||||||||||||||||||||||||
Qy   1453 GAGCTGTGAAGCCTTGAGAGTAATGGCTAAAATTATGAGAGAATGTTGGTATGCCAATGG 1512
```

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Db   1470 agcagctaggctgacagctttgcgaattaaaaaaacattgtcacagctcagccaacagga 1529
           |||||||||||| ||||| ||||| ||||| |||||||| || || ||||| ||||||||
Qy   1513 AGCAGCTAGGCTTACAGCATTGCGGATTAAGAAAACATTATCGCAACTCAGTCAACAGGA 1572

Db   1530 aggcatcaaaatgtaa 1545
           ||||||||||||||||
Qy   1573 AGGCATCAAAATGTAA 1588
```

RESULT 9
LOCUS CHKRPK2 2186 bp mRNA VRT 09-DEC-1993
DEFINITION Chicken RPK-2 mRNA for receptor protein kinase, complete cds.
ACCESSION D14460
NID g285699
KEYWORDS TGF-beta receptor-related; receptor protein kinase; serine/threonine kinase; transmembrane protein.
SOURCE Gallus gallus (library: lambda gt10) stage 24-26 (Hamburger & Hamilton) cDNA to mRNA, clones S5 and S7.
ORGANISM Gallus gallus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 2186)
AUTHORS Nohno,T., Sumitomo,S., Ishikawa,T., Ando,C., Nishida,S., Noji,S. and Saito,T.
TITLE Nucleotide sequence of a cDNA encoding the chicken receptor protein kinase of the TGF-beta receptor family
JOURNAL DNA Seq. 3 (6), 393-396 (1993)
MEDLINE 94033626

Query Match 36.1%; Score 833; DB 49; Length 2186;
Best Local Similarity 82.1%; Pred. No. 0.00e+00;
Matches 1181; Conservative 0; Mismatches 240; Indels 18; Gaps 7;

RESULT 13
LOCUS HSALK4A 2333 bp RNA PRI 29-SEP-1993
DEFINITION Homo sapiens ALK-4 mRNA, complete CDS.
ACCESSION Z22536
NID g402188
KEYWORDS ALK-4 gene; cell surface receptor; serine threonine kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2333)
AUTHORS ten Dijke,P.P.
TITLE Direct Submission
JOURNAL Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3, Uppsala, S-751 24, Sweden
REFERENCE 2 (bases 1 to 2333)
AUTHORS ten Dijke,P., Ichijo,H., Franzen,P., Schulz,P., Saras,J., Toyoshima,H., Heldin,C.H. and Miyazono,K.
TITLE Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity
JOURNAL Oncogene 8 (10), 2879-2887 (1993)
MEDLINE 93390967

Query Match 20.8%; Score 481; DB 70; Length 2333;
Best Local Similarity 74.8%; Pred. No. 0.00e+00;
Matches 725; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 04:43:27 1997; MasPar time 220.72 Seconds
967.382 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308

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N.A. Sequence:      1 GGCGAGGCGAGGTTTGCTGG.....TGTTAAAACCTATAGTGTTT 2308
     Comp:            CCGCTCCGCTCCAAACGACC.....ACAATTTTGGATATCACAAA
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Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.949; Variance 6.392; scale 1.557

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	2280	98.8	2308	11	Q66638	Human Activin recepto	0.00e+00
2	1163	50.4	1794	14	Q83534	Sequence encoding ser	0.00e+00
3	1102	47.7	1506	22	T36068	Mullerian inhibiting	0.00e+00
4	1102	47.7	1506	8	Q49766	Misr4.	0.00e+00
5	481	20.8	2333	11	Q66637	Human Activin recepto	2.37e-290
6	471	20.4	1518	8	Q49764	Misr2A/misr2B.	1.01e-283
7	471	20.4	2160	11	Q66641	Mouse Activin recepto	1.01e-283
8	467	20.2	1647	14	Q83533	Sequence encoding ser	4.50e-281
9	462	20.0	1506	22	T36070	Mullerian inhibiting	9.23e-278
10	445	19.3	1482	20	T26994	Serine threonine kina	1.67e-266

ALIGNMENTS

RESULT 1
ID Q66638 standard; cDNA; 2308 BP.
AC Q66638;
DT 20-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 5 (hALK-5) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 5'UTR 1..76
FT /*tag= a
FT /note= "contains an in-frame stop codon at
FT nucleotides (-54)-(-52)"
FT CDS 77..1588
FT /*tag= b
FT /product= activin receptor-like kinase 5
FT 3'UTR 1589..2308
FT /*tag= c
FT /note= "3'UTR is a total of 3.7kb and was not
FT completely sequenced"
PN WO9411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.

PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.

RESULT 2
ID Q83534 standard; DNA; 1794 BP.
AC Q83534;
DT 28-SEP-1995 (first entry)
DE Sequence encoding serine/threonine kinase receptor W120.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 83..1594
FT /*tag= a
FT /product= Serine/threonine kinase receptor.
PN WO9507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR P-PSDB; R70241.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 3; Page 64-66; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 1794 BP; 488 A; 390 C; 454 G; 462 T;

Query Match 50.4%; Score 1163; DB 14; Length 1794;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1481; Conservative 0; Mismatches 156; Indels 27; Gaps 11;

RESULT 3
T36068 standard; cDNA; 1506 BP.
AC T36068;
DT 30-OCT-1996 (first entry)
DE Mullerian inhibiting substance receptor coding sequence misr4.
KW Mullerian inhibiting substance receptor; MISR; TGF-beta receptor;
KW transforming growth factor beta type I receptor; gene therapy;
KW wound healing; tumour treatment; rat inhibin; ds.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 1..1506
FT /*tag= a
FT /product= MISR4
PN US5538892-A.
PD 23-JUL-1996.
PF 18-MAR-1992; 853396.
PR 18-MAR-1992; US-853396.
PR 11-MAR-1993; US-029673.
PR 04-NOV-1993; US-149105.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYDU-) UNIV DUKE.
PI Donahoe PK, Gustafson M, He W, Wang X;
DR WPI; 96-353830/35.
DR P-PSDB; W03758.
PT New isolated TGF-beta type I receptor DNA - used to develop prods
PT for diagnosis and therapy, e.g. for treating tumours or promoting
PT wound healing
PS Claim 1; Columns 33-36; 44pp; English.
CC Degenerate PCR primers were designed based on two highly conserved
CC regions within the cDNA encoding a murine activin receptor, human
CC and porcine TGF-beta type II receptor and the daf-1 receptor of
CC C.elegans. The primers (see T36072 and T36073) were used for
CC amplifying clones present in a 14.5 day foetal rat urogenital ridge
CC cDNA COS cell expression library. Four clones encoding portions of
CC four novel polypeptides (all putative serine/threonine kinases)
CC were obtained and designated pGEM7-Misr1, 2, 3 and 4. The inserts
CC from these clones were used as probes to isolate full-length cDNA
CC sequences for each of the four TGF-beta type I receptors. Misr1 is
CC believed to encode an isoform of the rat Mullerian Inhibiting
CC Substance (MIS) receptor, while misr2A/misr2B, misr3 and misr4 are
CC believed to encode monomeric isoforms of the rat inhibin receptor
CC and/or BMP receptor. The present sequence is misr4; isolated DNA
CC able to hybridise to this sequence under stringent conditions is
CC claimed.
SQ Sequence 1506 BP; 428 A; 321 C; 363 G; 394 T;

Query Match 47.7%; Score 1102; DB 22; Length 1506;
Best Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;

RESULT 4
ID Q49766 standard; cDNA; 1506 BP.
AC Q49766;
DT 20-APR-1994 (first entry)
DE Misr4.
KW MIS; Mullerian Inhibitory Substance; receptor;
KW transforming growth factor; inhibin; BMP;
KW membrane serine/threonine kinase receptor;
KW bone morphogenesis protein; ss.
OS Rattus rattus.
PN WO9319177-A.
PD 30-SEP-1993.
PF 15-MAR-1993; U02387.
PR 18-MAR-1992; US-853396.
PR 11-MAR-1993; US-029673.
PA (GEHO) GEN HOSPITAL CORP.
PI Donahoe PK, Gustafson M, He WW;
DR WPI; 93-320743/40.
DR P-PSDB; R41923.
PT New receptors of the transforming growth factor-beta receptor
PT family - comprising Mullerian Inhibitory Substance Receptors and
PT inhibin receptors
PS Claim 53; Fig 4; 59pp; English.
CC Misr1 (Q49763) is believed to encode an isoform of the rat
CC MIS receptor. Misr2A/misr2B (Q49764), misr3 (Q49765) and misr4
CC (Q49766) are believed to encode monomeric isoforms of the rat
CC inhibin receptor and/or BMP receptor.
SQ Sequence 1506 BP; 428 A; 321 C; 363 G; 394 T;

Query Match 47.7%; Score 1102; DB 8; Length 1506;
Best Local Similarity 88.9%; Pred. No. 0.00e+00;
Matches 1294; Conservative 0; Mismatches 156; Indels 6; Gaps 5;

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 04:47:38 1997; MasPar time 1458.40 Seconds
1014.493 Million cell updates/sec
Tabular output not generated.

Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GGCGAGGCGAGGTTTGCTGG.....TGTTAAAACCTATAGTGTTT 2308
Comp: CCGCTCCGCTCCAAACGACC.....ACAATTTTGGATATCACAAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	720	31.2	720	196	G06514	human STS WI-7314.	0.00e+00
2	332	14.4	426	8	AA047142	zk74e04.r1 Soares pre	0.00e+00
3	332	14.4	426	230	HSA47142	zk74e04.r1 Soares pre	0.00e+00
4	132	5.7	739	10	AA053838	zf53c07.r1 Soares ret	3.47e-210
5	132	5.7	739	231	HSA53838	zf53c07.r1 Soares ret	3.47e-210
6	114	4.9	515	43	C17679	Human placenta cDNA 5	4.04e-172
7	114	4.9	515	239	HSC6799	Human placenta cDNA 5	4.04e-172
8	96	4.2	404	165	W39552	zc18g04.r1 Soares par	9.48e-135
9	92	4.0	631	168	W48139	mc85f09.r1 Soares mou	1.45e-126
10	87	3.8	471	164	W34981	mc33h08.r1 Soares mou	2.08e-116

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 05:12:37 1997; MasPar time 86.86 Seconds
854.056 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-9
Description: (1-2308) from US08436265.seq
Perfect Score: 2308
N.A. Sequence: 1 GGCGAGGCGAGGTTTGCTGG.....TGTTAAAACCTATAGTGTTT 2308
Comp: CCGCTCCGCTCCAAACGACC.....ACAATTTTGGATATCACAAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 60653 seqs, 16071407 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:51 2:52 3:53 4:54 5:55 6:56 7:PCT90 8:PCT91 9:PCT92
10:PCT93 11:PCT94 12:PCT95 13:PCT96

Statistics: Mean 9.385; Variance 5.413; scale 1.734

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1163	50.4	1794	11	PCT-US94-1	Sequence 9, Applicatio	0.00e+00
2	1102	47.7	1506	5	US-08-149-	Sequence 4, Applicatio	0.00e+00
3	1102	47.7	1506	5	US-08-317-	Sequence 4, Applicatio	0.00e+00
4	467	20.2	1647	11	PCT-US94-1	Sequence 7, Applicatio	0.00e+00
5	462	20.0	1506	5	US-08-149-	Sequence 2, Applicatio	0.00e+00
6	462	20.0	1506	5	US-08-317-	Sequence 2, Applicatio	0.00e+00
7	445	19.3	1482	6	US-08-341-	Sequence 1, Applicatio	4.51e-299
8	262	11.4	2076	11	PCT-US94-1	Sequence 3, Applicatio	8.90e-165
9	261	11.3	2932	12	PCT-US95-0	Sequence 5, Applicatio	4.75e-164
10	245	10.6	1813	11	PCT-US94-1	Sequence 1, Applicatio	2.03e-152

ALIGNMENTS

RESULT 1
ID PCT-US94-10080-9 STANDARD; DNA; UNC; 1794 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 9, Application PC/TUS9410080.
CC Sequence 9, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
Query Match 50.4%; Score 1163; DB 11; Length 1794;
Best Local Similarity 89.0%; Pred. No. 0.00e+00;
Matches 1481; Conservative 0; Mismatches 156; Indels 27; Gaps 11;

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:58:06 1997; MasPar time 10.36 Seconds
529.135 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-10
Description: (1-503) from US08436265.pep
Perfect Score: 3687
Sequence: 1 MEAAVAAPRPRLLLLVLAAA.....TALRIKKTLSQLSQQEGIKM 503

Scoring table: PAM 150
Gap 11

Searched: 92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19

Statistics: Mean 35.793; Variance 157.139; scale 0.228

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3657	99.2	503	10	R55370	Human Activin recepto	0.00e+00
2	3493	94.7	503	13	R70241	Serine/threonine kina	0.00e+00
3	3454	93.7	501	18	W03758	Mullerian inhibiting	0.00e+00
4	3454	93.7	501	8	R41923	MISR4.	0.00e+00
5	2517	68.3	505	13	R70240	Serine/threonine kina	7.49e-229
6	2517	68.3	505	10	R55373	Mouse Activin recepto	7.49e-229
7	2516	68.2	505	8	R41921	MISR2A/MISR2B.	9.38e-229
8	2515	68.2	505	10	R55369	Human Activin recepto	1.17e-228
9	2481	67.3	501	18	W03760	Mullerian inhibiting	2.46e-225
10	2384	64.7	493	17	R95562	Serine threonine kina	7.30e-216

ALIGNMENTS

RESULT 1
ID R55370 standard; Protein; 503 AA.
AC R55370;
DT 20-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 5 (hALK-5).

KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= putative signal peptide
FT Protein 25..503
FT /label= activin receptor-like kinase 5
FT /note= "mature protein"
PN WO9411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR [illegible]-MAR-1993; GB-004677.
PR [illegible]-MAR-1993; GB-004680.
PR 26-MAY-1993; GB-011047.
PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.

Query Match 99.2%; Score 3657; DB 10; Length 503;
Best Local Similarity 99.4%; Pred. No. 0.00e+00;
Matches 500; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Db      1 meaavaaprprllllvlaaaaaaaaallpgatalqcfchlctkdnftcvtdglcfvsvte 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db     61 ttdkvihnsmciaeidliprdrpfvcapssktrsvtttyccnqdhcnkielpttvksspg 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTTVKSSPG 120

Db    121 lgpvelaaviagpvcfvcislmlmvyichnrtvihhrvpneedpsldrpfisegttlkdl 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 LGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTTLKDL 180

Db    181 iydmttsgsgsrlpllvqrtiartivlqesigkgrfgevwrgkwrgeevavnifssreer 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 IYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREER 240

Db    241 swfreaeiygtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnrytvtve 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 SWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVE 300

Db    301 gmiklalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglavrhds 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 GMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDS 360

Db    361 atdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcsiggi 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 ATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGI 420

Db    421 hedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwyanga 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 HEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGA 480

Db    481 arltalrikktlsqlsqqegikm 503
          |||||||||||||||||||||||
Qy    481 ARLTALRIKKTLSQLSQQEGIKM 503
```

RESULT 2
ID R70241 standard; Protein; 503 AA.
AC R70241;
DT 28-SEP-1995 (first entry)
DE Serine/threonine kinase receptor W120.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition.
OS Mus musculus.

PN WO9507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR N-PSDB; Q83534.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 26; Page 67-68; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 503 AA;

Query Match 94.7%; Score 3493; DB 13; Length 503;
Best Local Similarity 95.7%; Pred. No. 0.00e+00;
Matches 485; Conservative 5; Mismatches 9; Indels 8; Gaps 3;

```
Db      1 meaaaaaprrpqllivlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte 56
          |||| ||||   ||:|| |||:    ||||| |||||||||||||||| ||||||||||
Qy      1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db     57 ttdkvihnsmciaeidliprdrpfvcapssktgavtttyccnqdhcnkielpttgpfsek 116
          |||||||||||||||||||||||||||||:||||||||||||||||||||     |
Qy     61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K 116

Db    117 qsaglgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegtt 176
           |:|||||||||||||||:||||||||||||||||||||||||||||||||||||||||||
Qy    117 SSPGLGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 176

Db    177 lkdliydmttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifss 236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 236

Db    237 reerswfreaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnryt 296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    237 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296

Db    297 vtvegmiklalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglav 356
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    297 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 356

Db    357 rhdsatdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcs 416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    357 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 416

Db    417 iggihedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwy 476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476

Db    477 angaarltalrikktlsqlsqqegikm 503
          |||||||||||||||||||||||||||
Qy    477 ANGAARLTALRIKKTLSQLSQQEGIKM 503
```

RESULT 3
ID W03758 standard; Protein; 501 AA.
AC W03758;
DT 30-OCT-1996 (first entry)
DE Mullerian inhibiting substance receptor MISR4.
KW Mullerian inhibiting substance receptor; MISR; TGF-beta receptor;
KW transforming growth factor beta type I receptor; gene therapy;

KW wound healing; tumour treatment; rat inhibin.
OS Rattus sp.
FH Key Location/Qualifiers
FT Binding_site 210..230
FT /label= ATP_binding_site
FT /note= "corresponds to conserved GXGXXGXVX(11-28)K
FT motif found in all serine/threonine kinases
FT and thought to form an ATP binding site"
PN US5538892-A.
PD 23-JUL-1996.
PF 18-MAR-1992; 853396.
PR 18-MAR-1992; US-853396.
PR 11-MAR-1993; US-029673.
PR 04-NOV-1993; US-149105.
PA [illegible] GEN HOSPITAL CORP.
PA (UYDU-) UNIV DUKE.
PI Donahoe PK, Gustafson M, He W, Wang X;
DR WPI; 96-353830/35.
DR N-PSDB; T36068.

Query Match 93.7%; Score 3454; DB 18; Length 501;
Best Local Similarity 95.3%; Pred. No. 0.00e+00;
Matches 483; Conservative 5; Mismatches 9; Indels 10; Gaps 4;

Db 1 meaasaalrrclllivlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte 56
Qy 1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db 57 ttdkvihnsmciaeidliprdrpfvcapssktgavt--yccnqdhcnkielpttgpfsek 114
Qy 61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K 116

Db 115 qsaglgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegtt 174
Qy 117 SSPGLGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 176

Db 175 lkdliydmttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifss 234
Qy 177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 236

Db 235 reerswfreaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnryt 294
Qy 237 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296

Db 295 vtvegmiklalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglav 354
Qy 297 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 356

Db 355 rhdsatdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcs 414
Qy 357 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 416

Db 415 iggihedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwy 474
Qy 417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476

Db 475 angaarltalrikktlsqlsqqegikm 501
Qy 477 ANGAARLTALRIKKTLSQLSQQEGIKM 503

RESULT 4
ID R41923 standard; Protein; 501 AA.
AC R41923;
DT 20-APR-1994 (first entry)
DE MISR4.

RESULT 5
ID R70240 standard; Protein; 505 AA.
AC R70240;
DT 28-SEP-1995 (first entry)
DE Serine/threonine kinase receptor W101.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition.
OS Mus musculus.
PN WO9507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR N-PSDB; Q83533.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 25; Page 63-64; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 505 AA;

Query Match 68.3%; Score 2517; DB 13; Length 505;
Best Local Similarity 71.2%; Pred. No. 7.49e-229;
Matches 356; Conservative 62; Mismatches 65; Indels 17; Gaps 14;

RESULT 6
ID R55373 standard; Protein; 505 AA.
AC R55373;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 4 (mALK-4).
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis.
OS Mus musculus.
PN WO9411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.
PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.
Query Match 68.3%; Score 2517; DB 10; Length 505;
Best Local Similarity 71.2%; Pred. No. 7.49e-229;
Matches 356; Conservative 62; Mismatches 65; Indels 17; Gaps 14;

Db 13 lvvlllagsggsgp-rgiqallcactsclqtnytcetdgacmvsifnl-dgvehhvrtci 70
Qy 14 LLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHN-SMCI 72

Db 71 pkvelvpagkpfycl-sse--dlrnthccyidfcnkidlrvpsghlkepahpsmwgpvel 127
Qy 73 AEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIEL--PTT-VK-SS-PGL-GPVEL 126

Db 128 vgiiagpvfllfliiiivflvinyhqr-vyhnrqrldmedpscemc-lskdktlqdlvyd 185
Qy 127 AAVIAGPVC--FVCISLMLMVYICHNRTVIHHRVPNE-EDPSLDRPFISEGTTLKDLIYD 183

Db 186 lstsgsgsglplfvqrtvartivlqeiigkgrfgevwrgrwrggdvavkifssreerswf 245
Qy 184 MTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWF 243

Db 246 reaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnrytvtiegmi 305

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        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
Qy    244 REAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMI 303

Db    306 klalsaasglahlhmeivgtqgkpgiahrdlksknilvkkngmcaiadlglavrhdavtd 365
        |||||:|||||||||||||||||:|||||||||||||||| | ||||||||||: ||
Qy    304 KLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATD 363

Db    366 tidiapnqrvgtkrymapevldetinmkhfdsfkcadiyalglvyweiarrcnsggvhed 425
        |||||||:|||||||||||||::||||||:||| |||||:|||:|||||||: ||:|||
Qy    364 TIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHED 423

Db    426 yqlpyydlvpsdpsieemrkvvcdqklrpnvpnwwqsyealrvmgkmmrecwyangaarl 485
        |||||||||||||:||||||||:||||||:||:||| |||||||:|:||||||||||||
Qy    424 YQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARL 483

Db    486 talrikktlsqlsvqedvki 505
        |||||||||||||| || :|:
Qy    484 TALRIKKTLSQLSQQEGIKM 503
```

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:58:55 1997; MasPar time 18.25 Seconds
785.825 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-10
Description: (1-503) from US08436265.pep
Perfect Score: 3687
Sequence: 1 MEAAVAAPRPRLLLLVLAAA.....TALRIKKTLSQLSQQEGIKM 503

Scoring table: PAM 150
Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir50
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 48.912; Variance 115.163; scale 0.425

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3687	100.0	503	13	A49432	activin receptor-lik	0.00e+00
2	3536	95.9	499	14	JC2062	transforming growth	0.00e+00
3	3493	94.7	503	14	JC2061	transforming growth	0.00e+00
4	3020	81.9	440	13	A56693	receptor protein kin	0.00e+00
5	2522	68.4	505	13	I38859	activin receptor Act	0.00e+00
6	2522	68.4	505	13	I37164	ALK-4 - human	0.00e+00
7	2516	68.2	505	14	I53417	type I serine-threon	0.00e+00
8	2204	59.8	476	13	I80182	activin type I recep	0.00e+00
9	2021	54.8	601	12	A55921	serine/threonine kin	0.00e+00
10	1893	51.3	487	13	I80183	activin type I recep	0.00e+00

```
RESULT    1
ENTRY             A49432     #type complete
TITLE             activin receptor-like kinase 5 precursor - human
ALTERNATE_NAMES   TGFbeta type I receptor ALK-5
CONTAINS          protein kinase (EC 2.7.1.37)
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                    08-Dec-1995
ACCESSIONS        A49432
REFERENCE         A49432
   #authors       Franzen, P.; ten Dijke, P.; Ichijo, H.; Yamashita, H.;
                    Schulz, P.; Heldin, C.H.; Miyazono, K.
   #journal       Cell (1993) 75:681-692
   #title         Cloning of a TGFbeta type I receptor that forms a heteromeric
                    complex with the TGFbeta type II receptor.
   #accession     A49432
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-503 ##label FRA
      ##cross-references GB:L11695
CLASSIFICATION    #superfamily protein kinase homology
KEYWORDS          glycoprotein; phosphotransferase; transmembrane protein
FEATURE
   203-499             #domain protein kinase homology #label KIN
SUMMARY           #length 503  #molecular-weight 55959  #checksum 1518

  Query Match           100.0%;  Score 3687;  DB 13;  Length 503;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   503;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
RESULT    2
ENTRY             JC2062     #type complete
TITLE             transforming growth factor-beta type I receptor precursor -
                    mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change
                    08-Dec-1995
ACCESSIONS        JC2062
REFERENCE         JC2062
   #authors       Suzuki, A.; Shioda, N.; Maeda, T.; Tada, M.; Ueno, N.
   #journal       Biochem. Biophys. Res. Commun. (1994) 198:1063-1069
   #title         A mouse TGF-beta type I receptor that requires type II
                    receptor for ligand binding.
   #accession     JC2062
      ##molecule_type mRNA
      ##residues       1-499 ##label SUZ
CLASSIFICATION    #superfamily protein kinase homology
FEATURE
   1-19                #domain signal sequence #status predicted #label SIG\
   20-499              #product transforming growth factor-beta type I receptor
                         #label MAT\
   122-145             #domain transmembrane #status predicted #label TMM\
   199-495             #domain protein kinase homology #label KIN\
   202-493             #domain intracellular kinase #label INK\
   41,146,266,340      #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 499  #molecular-weight 55790  #checksum 157

  Query Match           95.9%;  Score 3536;  DB 14;  Length 499;
  Best Local Similarity 96.4%;  Pred. No. 0.00e+00;
  Matches   485;  Conservative    5;  Mismatches   9;  Indels   4;  Gaps   1;

Db      1 meaaaaaprrpqllivlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte 56
          |||| ||||   ||:|| |||:    ||||| |||||||||||||||| ||||||||||
Qy      1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db     57 ttdkvihnsmciaeidliprdrpfvcapssktgavtttyccnqdhcnkielpttekqsag 116
          |||||||||||||||||||||||||||||:|||||||||||||||||||| | |:|
Qy     61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTTVKSSPG 120

Db    117 lgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegttlkdl 176
          |||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Qy    121 LGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTTLKDL 180

Db    177 iydmttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifssreer 236
```

```
Qy    181 IYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREER 240

Db    237 swfreaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnrytvtve 296

Qy    241 SWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVE 300

Db    297 gmiklalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglavrhds 356

Qy    301 GMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDS 360

Db    357 atdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcsiggi 416

Qy    361 ATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGI 420

Db    417 hedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqsealrvmakimrecwyanga 476

Qy    421 HEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGA 480

Db    477 arltalrikktlsqlsqqegikm 499

Qy    481 ARLTALRIKKTLSQLSQQEGIKM 503
```

RESULT 3
ENTRY JC2061 #type complete
TITLE transforming growth factor-beta type I receptor, ESK 2 precursor - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Dec-1995
ACCESSIONS JC2061
REFERENCE JC2061
#authors Tomoda, T.; Kudoh, T.; Noma, T.; Nakazawa, A.; Muramatsu, M.; Arai, K.
#journal Biochem. Biophys. Res. Commun. (1994) 198:1054-1062
#title Molecular cloning of a mouse counterpart for human TGF-beta type I receptor.
#accession JC2061
##molecule_type mRNA
##residues 1-503 ##label TOM
COMMENT This protein is the mouse counterpart for human transforming growth factor beta RI.
CLASSIFICATION #superfamily protein kinase homology
KEYWORDS glycoprotein; receptor; transmembrane protein
FEATURE
[redacted]20 #domain signal sequence #status predicted #label SIG\
[redacted]-501 #product transforming growth factor-beta type I receptor ESK 2 #status predicted #label MAT\
126-147 #domain transmembrane #status predicted #label TMM\
203-499 #domain protein kinase homology #label KIN\
41 #binding_site carbohydrate (Asn) (covalent) #status predicted
SUMMARY #length 503 #molecular-weight 56178 #checksum 2259

Query Match 94.7%; Score 3493; DB 14; Length 503;
Best Local Similarity 95.7%; Pred. No. 0.00e+00;
Matches 485; Conservative 5; Mismatches 9; Indels 8; Gaps 3;

```
Db      1 meaaaaaprrpqllivlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte 56

Qy      1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db     57 ttdkvihnsmciaeidliprdrpfvcapssktgavtttyccnqdhcnkielpttgpfsek 116

Qy     61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K 116

Db    117 qsaglgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegtt 176

Qy    117 SSPGLGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 176

Db    177 lkdliydmttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifss 236

Qy    177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 236

Db    237 reerswfreaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnryt 296

Qy    237 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296

Db    297 vtvegmiklalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglav 356

Qy    297 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 356

Db    357 rhdsatdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcs 416

Qy    357 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 416

Db    417 iggihedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwy 476

Qy    417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476

Db    477 angaarltalrikktlsqlsqqegikm 503

Qy    477 ANGAARLTALRIKKTLSQLSQQEGIKM 503
```

RESULT 4
ENTRY A56693 #type complete
TITLE receptor protein kinase RPK-2 - chicken
ORGANISM #formal_name Gallus gallus #common_name chicken
DATE 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 08-Dec-1995
ACCESSIONS A56693
REFERENCE A56693
#authors Nohno, T.; Sumitomo, S.; Ishikawa, T.; Ando, C.; Nishida, S.; Noji, S.; Saito, T.
#journal DNA Seq. (1993) 3:393-396
#title Nucleotide sequence of a cDNA encoding the chicken receptor protein kinase of the TGF-beta receptor family.
#accession A56693
##status preliminary
##molecule_type mRNA
##residues 1-440 ##label NOH
##cross-references GB:D14460
CLASSIFICATION #superfamily protein kinase homology
KEYWORDS transmembrane protein
FEATURE
140-436 #domain protein kinase homology #label KIN
SUMMARY #length 440 #molecular-weight 49516 #checksum 7044

Query Match 81.9%; Score 3020; DB 13; Length 440;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 413; Conservative 11; Mismatches 10; Indels 6; Gaps 2;

```
Db      1 mciaeidliprdrpficapsfrdgvttlphccdrdhcnkielpiptpgptpgrpasslgp 60

Qy     70 MCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPT-TVKSSPG-----LGP 123

Db     61 velaaviagpvcfvcislmlilylchnrtvihhrvpseedpsldrpfisegttlkdliyd 120

Qy    124 VELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTTLKDLIYD 183

Db    121 mttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifssreerswf 180

Qy    184 MTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWF 243

Db    181 reaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnrytvtvegmi 240

Qy    244 REAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMI 303

Db    241 klalstasglahlhmeivgtqgkpaiahrdlksknilvkkngtcciadlglavrhdsatd 300
```

```
Qy    304 KLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATD 363

Db    301 tidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcsiggihed 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    364 TIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHED 423

Db    361 yqlpyydlvpsdpsveemkkvvceqklrpnipnrwqscealrvmakimrecwyangaarl 420
          ||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Qy    424 YQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARL 483

Db    421 talrikktlsqlsqqegikm 440
          ||||||||||||||||||||
Qy    484 TALRIKKTLSQLSQQEGIKM 503
```

```
RESULT    5
ENTRY             I38859     #type complete
TITLE             activin receptor ActR-IB, type I - human
ALTERNATE_NAMES   ALK-4 protein
ORGANISM          #formal_name Homo sapiens #common_name man
DATE              16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
                    12-Apr-1996
ACCESSIONS        I38859; S37184
REFERENCE         A56060
   #authors       Carcamo, J.; Weis, F.M.; Ventura, F.; Wieser, R.; Wrana,
                    J.L.; Attisano, L.; Massague, J.
   #journal       Mol. Cell. Biol. (1994) 14:3810-3821
   #title         Type I receptors specify growth-inhibitory and
                    transcriptional responses to transforming growth factor
                    beta and activin.
   #cross-references MUID:94254839
   #accession     I38859
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-505 ##label RES
      ##cross-references EMBL:U14722; NID:g555933; CDS_PID:g555934
REFERENCE         S37181
   #authors       ten Dijke, P.P.; Ichijo, H.H.; Franzen, P.P.; Schulz, P.P.;
                    Saras, J.J.; Toyoshima, H.H.; Heldin, C.C.; Miyazono, K.K.
   #submission    submitted to the EMBL Data Library, April 1993
   #description   Activin receptor-like kinases, A novel subclass of cell
                    surface receptors with predicted serine/threonine kinase
                    activity.
   #accession     S37184
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-505 ##label TEN
      ##cross-references EMBL:Z22536
CLASSIFICATION    #superfamily protein kinase homology
FEATURE
   205-501             #domain protein kinase homology #label KIN
SUMMARY           #length 505  #molecular-weight 56806  #checksum 3363

  Query Match           68.4%;  Score 2522;  DB 13;  Length 505;
  Best Local Similarity  70.7%;  Pred. No. 0.00e+00;
  Matches   353;  Conser
RESULT    9
ENTRY             A55921     #type complete
TITLE             serine/threonine kinase Atr-1 - fruit fly (Drosophila
                    melanogaster)
ORGANISM          #formal_name Drosophila melanogaster
DATE              08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change
                    08-Dec-1995
ACCESSIONS        A55921
REFERENCE         A55921
   #authors       Wrana, J.L.; Tran, H.; Attisano, L.; Arora, K.; Childs, S.R.;
                    Massague, J.; O'Connor, M.B.
   #journal       Mol. Cell. Biol. (1994) 14:944-950
   #title         Two distinct transmembrane serine/threonine kinases from
                    Drosophila melanogaster form an activin receptor complex.
   #accession     A55921
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-601 ##label WRA
      ##cross-references GB:U04692
CLASSIFICATION    #superfamily protein kinase homology
FEATURE
   301-597             #domain protein kinase homology #label KIN
SUMMARY           #length 601  #molecular-weight 67219  #checksum 801

  Query Match           54.8%;  Score 2021;  DB 12;  Length 601;
  Best Local Similarity  58.6%;  Pred. No. 0.00e+00;
  Matches   279;  Conservative   77;  Mismatches 111;  Indels   9;  Gaps   8;
```

```
RESULT   11
ENTRY             A53444     #type complete
TITLE             activin receptor-like kinase 6 precursor - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1994 #sequence_revision 19-May-1994 #text_change
                    08-Dec-1995
ACCESSIONS        A53444; S40159
REFERENCE         A53444
   #authors       ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho,
                    M.; Miyazono, K.; Heldin, C.H.
   #journal       Science (1994) 264:101-104
   #title         Characterization of type I receptors for transforming growth
                    factor-beta and activin.
   #accession     A53444
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-502 ##label TEN
      ##cross-references GB:Z23143
REFERENCE         S40158
   #authors       Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.;
                    ten Dijke, P.
   #submission    submitted to the EMBL Data Library, June 1993
   #description   ALK-3 and ALK-6: the closely related members in the
                    serine/threonine kinase receptor family.
   #accession     S40159
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-502 ##label MIY
      ##cross-references EMBL:Z23143
CLASSIFICATION    #superfamily protein kinase homology
FEATURE
   202-498             #domain protein kinase homology #label KIN
SUMMARY           #length 502  #molecular-weight 56944  #checksum 5099

  Query Match           48.6%;  Score 1793;  DB 14;  Length 502;
  Best Local Similarity  54.0%;  Pred. No. 1.36e-287;
  Matches   266;  Conservative   84;  Mismatches 124;  Indels  19;  Gaps  15;

Db     18 gestaptprpkilrckchhhcpedsvnnicstdgycftmieeddsgmpvvtsgclg-le- 75
          : ::|  | :  |:| ||  |  |  |  | ||| ||  : |  : : :  | |:: ::
Qy     22 AAAAALLPGATALQCFCHL-CTKD--NFTCVTDGLCFVSVTET-TDKVIHNSMCIAEIDL 77

Db     76 -gsd--fqcrdtpiphqrrsieccternecnk-dlhptlpplkdrdfvdgpihhkallis 131
             |  | |  ::      :  || : : ||| :| ||   :|    : ||:   |: |:
Qy     78 IPRDRPFVCAPSSKTGSVTTTYCCNQ-DHCNKIEL-PT--TVKSSPGL-GPVELAAV-IA 131

Db    132 vtvcsl-l-lvliilfcyfrykrqearprysigleqdetyippgeslrdlieqsqssgsg 189
            || : : |:|:: :|  |   :  |          |  :|: | :|:||| :  :|||| 
Qy    132 GPVCFVCISLMLMVYICHNRTVIHH-RVPNEEDPSLDRPFISEGTTLKDLIYDMTTSGSG 190

Db    190 sglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeaswfreteiyq 249
          ||||||||||||: | :   |||||:|||| |||||| ||||:| : || |||||:||||
Qy    191 SGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWFREAEIYQ 250

Db    250 tvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldaksmlklayssv 309
          ||::|||||||||||| |  |:|||| |::||||:|||:|||:  |:   :|:||| |:
```

```
Qy     251 TVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIKLALSTA 310

Db     310 sglchlhteifstqgkpaiahrdlksknilvkkngtcciadlglavkfisdtnevdippn 369
           ||| ||| || :|||||||||||||||||||||||||||||||:  | |: :||:||
Qy     311 SGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPN 370

Db     370 trvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiveeyqlpyhd 429
           ||||||||:|||||:|:| :||:|:  ||:|: ||::|||||||  ||| |:|||| |
Qy     371 HRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYD 430

Db     430 lvpsdpsyedmreivcmkklrpsfpnrwssdeclrqmgklmtecwaqnpasrltalrvkk 489
           |||||||  |:|| :||  ||||::|||| | | || |:|:| |||  | |:||||||:||
Qy     431 LVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKK 490

Db     490 tlakmsesqdikl 502
           ||: :|: : ||:
Qy     491 TLSQLSQQEGIKM 503

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:          Tue Jun 24 18:00:22 1997;  MasPar time 12.51 Seconds
                                            852.767 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-436-265-10
Description:     (1-503) from US08436265.pep
Perfect Score:   3687
Sequence:        1 MEAAVAAPRPRLLLLVLAAA.........TALRIKKTLSQLSQQEGIKM 503

Scoring table:   PAM 150
                 Gap 11

Searched:        59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        swiss-prot34
                   1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                   8:part8 9:part9 10:part10 11:part11

Statistics:      Mean 50.633;  Variance 86.716;  scale 0.584

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

Result          %
  No.  Score  Query Match Length DB  ID          Description            Pred. No.
 ---------------------------------------------------------------------------------
    1   3687   100.0     503   5  KIR4_HUMAN  SERINE/THREONINE-PROT  0.00e+00
    2   3454    93.7     501   5  KIR4_RAT    SERINE/THREONINE-PROT  0.00e+00
    3   2522    68.4     505   5  KIR2_HUMAN  SERINE/THREONINE-PROT  0.00e+00
    4   2516    68.2     505   5  KIR2_RAT    SERINE/THREONINE-PROT  0.00e+00
    5   1793    48.6     502   5  KIR6_MOUSE  SERINE/THREONINE-PROT  0.00e+00
    6   1792    48.6     502   5  KIR6_CHICK  SERINE/THREONINE-PROT  0.00e+00
    7   1770    48.0     532   5  KIR5_MOUSE  SERINE/THREONINE-PROT  0.00e+00
    8   1762    47.8     532   5  KIR5_HUMAN  SERINE/THREONINE-PROT  0.00e+00
    9   1651    44.8     509   5  KIR1_HUMAN  SERINE/THREONINE-PROT  0.00e+00
   10   1646    44.6     509   5  KIR1_RAT    SERINE/THREONINE-PROT  0.00e+00

                               ALIGNMENTS

RESULT    1
ID   KIR4_HUMAN     STANDARD;      PRT;   503 AA.
AC   P36897;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37)
DE   (SKR4) (ACTIVIN RECEPTOR-LIKE KINASE 5) (ALK-5) (TGF-BETA TYPE I
DE   RECEPTOR).
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94061986.
RA   FRANZEN P., TEN DIJKE P., ICHIJO H., YAMASHITA H., SCHULZ P.,
RA   HELDIN C.H., MIYAZONO K.;
RL   CELL 75:681-692(1993).
CC   -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC       COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC       SIGNAL TRANSDUCERS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED, MOST ABUNDANT
CC       IN PLACENTA AND LEAST ABUNDANT IN BRAIN AND HEART.
CC   -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC       PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
  Query Match          100.0%;  Score 3687;  DB 5;  Length 503;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches  503;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT    2
ID   KIR4_RAT       STANDARD;      PRT;   501 AA.
AC   P80204;
DT   01-OCT-1993 (REL. 27, CREATED)
DT   01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR (EC 2.7.1.37)
DE   (SKR4) (TGF-BETA TYPE I RECEPTOR).
OS   RATTUS NORVEGICUS (RAT).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; RODENTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=UROGENITAL RIDGE;
RX   MEDLINE; 93372378.
RA   HE W.-W., GUSTAFSON M., HIROBE S., DONAHOE P.;
RL   DEV. DYN. 196:133-142(1993).
CC   -!- FUNCTION: TYPE I/TYPE II TGF-BETA RECEPTORS FORM AN HETEROMERIC
CC       COMPLEX AFTER BINDING TGF-BETA AT THE CELL SURFACE AND ACT AS
CC       SIGNAL TRANSDUCERS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- TISSUE SPECIFICITY: UROGENITAL RIDGE, TESTIS, OVARY, BRAIN AND
CC       LUNGS.
CC   -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC       PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
DR   EMBL; L26110; G1113130; -.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM.
KW   RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW   TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    501       SERINE/THREONINE KINASE RECEPTOR R4.
FT   DOMAIN       23    123       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    124    146       POTENTIAL.
FT   DOMAIN      147    501       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      203    493       PROTEIN KINASE.
FT   NP_BIND     209    217       ATP (BY SIMILARITY).
FT   BINDING     230    230       ATP (BY SIMILARITY).
FT   ACT_SITE    331    331       BY SIMILARITY.
FT   CARBOHYD     41     41       POTENTIAL.
SQ   SEQUENCE   501 AA;  55999 MW;  67D99EAB CRC32;

  Query Match          93.7%;  Score 3454;  DB 5;  Length 501;
  Best Local Similarity 95.3%;  Pred. No. 0.00e+00;
  Matches  483;  Conservative    5;  Mismatches   9;  Indels  10;  Gaps   4;
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Db      1 meaasaalrrcllllvlvaaat----llpgakalqcfchlctkdnftcetdglcfvsvte 56
          |||| || |  |||:|| |||:    ||||| ||||||||||||||| ||||||||||
Qy      1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db     57 ttdkvihnsmciaeidliprdrpfvcapssktgavt--yccnqdhcnkielpttgpfsek 114
          ||||||||||||||||||||||||||||||:||  ||||||||||||||     |
Qy     61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K 116

Db    115 qsaglgpvelaaviagpvcfvcialmlmvyichnrtvihhrvpneedpsldrpfisegtt 174
          |:|||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Qy    117 SSPGLGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 176

Db    175 lkdliydmttsgsgsglpllvqrtiartivlqesigkgrfgevwrgkwrgeevavkifss 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 236

Db    235 reerswfreaeiyqtvmlrhenilgfiaadnkdngtwtqlwlvsdyhehgslfdylnryt 294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    237 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296

Db    295 vtvegmiklalstasglahlhmeivgtqgkpaiahrdlkskniivkkngtcciadlglav 354
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    297 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 356

Db    355 rhdsatdtidiapnhrvgtkrymapevlddsinmkhfesfkradiyamglvfweiarrcs 414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    357 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 416

Db    415 iggihedyqlpyydlvpsdpsveemrkvvceqklrpnipnrwqscealrvmakimrecwy 474
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Qy    417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476

Db    475 angaarltalrikktlsqlsqqegikm 501
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Qy    477 ANGAARLTALRIKKTLSQLSQQEGIKM 503
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RESULT    3
ID   KIR2_HUMAN     STANDARD;      PRT;   505 AA.
AC   P36896;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   SERINE/THREONINE-PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37)
DE   (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB).
GN   ACVRLK4.
OS   HOMO SAPIENS (HUMAN).
OC   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC   EUTHERIA; PRIMATES.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PLACENTA;
RX   MEDLINE; 93390967.
RA   TEN DIJKE P., ICHIJO H., FRANZEN P., SCHULZ P., SARAS J.,
RA   TOYOSHIMA H., HELDIN C.H., MIYAZONO K.;
RL   ONCOGENE 8:2879-2887(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE; 94254839.
RA   CARCAMO J., WEIS F.M., VENTURA F., WIESER R., WRANA J.L.,
RA   ATTISANO L., MASSAGUE J.;
RL   MOL. CELL. BIOL. 14:3810-3821(1994).
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC   -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC       PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
DR   EMBL; Z22536; G402189; -.
DR   EMBL; U14722; G555934; -.
DR   PIR; S37184; S37184.
DR   MIM; 601300; -.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM.
KW   RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW   TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    505       SERINE/THREONINE KINASE RECEPTOR R2.
FT   DOMAIN       24    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    149       POTENTIAL.
FT   DOMAIN      150    505       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      207    497       PROTEIN KINASE.
FT   NP_BIND     213    221       ATP (BY SIMILARITY).
FT   BINDING     234    234       ATP (BY SIMILARITY).
FT   ACT_SITE    335    335       BY SIMILARITY.
FT   CARBOHYD     43     43       POTENTIAL.
SQ   SEQUENCE   505 AA;  56806 MW;  85564CF7 CRC32;

  Query Match           68.4%;  Score 2522;  DB 5;  Length 505;
  Best Local Similarity 70.7%;  Pred. No. 0.00e+00;
  Matches   353;  Conservative   62;  Mismatches  69;  Indels  15;  Gaps  11;

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:          Tue Jun 24 18:01:25 1997;  MasPar time 5.11 Seconds
                                            358.162 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-436-265-10
Description:     (1-503) from US08436265.pep
Perfect Score:   3687
Sequence:        1 MEAAVAAPRPRLLLLVLAAA.....TALRIKKTLSQLSQQEGIKM 503

Scoring table:   PAM 150
                 Gap 11

Searched:        39797 seqs, 3636180 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        a-issued
                   1:51 2:52 3:53 4:54 5:55 6:56 7:PCT90 8:PCT91 9:PCT92
                   10:PCT93 11:PCT94 12:PCT95 13:PCT96

Statistics:      Mean 33.610;  Variance 164.611;  scale 0.204

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                    %
Result              Query
  No.   Score       Match  Length DB  ID          Description            Pred. No.
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    1    3493        94.7     503 11  PCT-US94-1  Sequence 10, Applicati  7.01e-292
    2    3454        93.7     501  5  US-08-317-  Sequence 17, Applicati  1.88e-288
    3    3454        93.7     501  5  US-08-149-  Sequence 17, Applicati  1.88e-288
    4    2517        68.3     505 11  PCT-US94-1  Sequence 8, Applicatio  3.61e-206
    5    2481        67.3     501  5  US-08-149-  Sequence 15, Applicati  5.17e-203
    6    2481        67.3     501  5  US-08-317-  Sequence 15, Applicati  5.17e-203
    7    2384        64.7     493  6  US-08-341-  Sequence 2, Applicatio  1.63e-194
    8    1793        48.6     502 12  PCT-US95-0  Sequence 8, Applicatio  7.87e-143
    9    1785        48.4     502 11  PCT-US94-1  Sequence 4, Applicatio  3.93e-142
   10    1769        48.0     532 11  PCT-US94-1  Sequence 2, Applicatio  9.77e-141

                          ALIGNMENTS

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ID   PCT-US94-10080-10     STANDARD;      PRT;   503 AA.
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AC   xxxxxx
XX
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DT   01-JAN-1900
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DE   Sequence 10, Application PC/TUS9410080.
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CC    Sequence 10, Application PC/TUS9410080
CC     GENERAL INFORMATION:
CC       APPLICANT:  GENETICS INSTITUTE, INC.
CC       TITLE OF INVENTION:  RECEPTOR PROTEINS
CC       NUMBER OF SEQUENCES:  19
  Query Match           94.7%;  Score 3493;  DB 11;  Length 503;
  Best Local Similarity  95.7%;  Pred. No. 7.01e-292;
  Matches   485;  Conservative    5;  Mismatches   9;  Indels   8;  Gaps   3;


RESULT    2
ID   US-08-317-847-17     STANDARD;     PRT;   501 AA.
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AC   xxxxxx
XX
DT   01-JAN-1900
XX
DE   Sequence 17, Application US/08317847.
XX
CC    Sequence 17, Application US/08317847
CC    Patent No. 5547854
CC     GENERAL INFORMATION:
CC       APPLICANT:  Donahoe, Patricia K.
CC       APPLICANT:  Gustafson, Michael
CC       APPLICANT:  He, Wei W.
CC       TITLE OF INVENTION:  FOUR NOVEL RECEPTORS OF THE TGF-B
CC       TITLE OF INVENTION:  FAMILY
CC       NUMBER OF SEQUENCES:  17
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Fish & Richardson
CC         STREET:  225 Franklin Street
CC         CITY:  Boston
CC         STATE:  Massachusetts
CC         COUNTRY:  U.S.A.
CC         ZIP:  02110-2804
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
CC         COMPUTER:  IBM PS/2 Model 50Z or 55SX
CC         OPERATING SYSTEM:  MS-DOS (Version 5.0)
CC         SOFTWARE:  WordPerfect (Version 5.1)
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/317,847
CC         FILING DATE:
CC         CLASSIFICATION:  435
CC       PRIOR APPLICATION DATA:
CC         APPLICATION NUMBER:  08/029,673
CC         FILING DATE:  March 11, 1993
CC         APPLICATION NUMBER:  07/853,396
CC         FILING DATE:  March 18, 1992
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Clark, Paul T.
CC         REGISTRATION NUMBER:  30,162
CC         REFERENCE/DOCKET NUMBER:  00786/127002
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (617) 542-5070
CC         TELEFAX:  (617) 542-8906
CC         TELEX:  200154
CC     INFORMATION FOR SEQ ID NO:  17:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  501
CC         TYPE:  amino acid
CC         STRANDEDNESS:
CC         TOPOLOGY:  linear
SQ   SEQUENCE   501 AA; 55999 MW; 1252583 CN;

  Query Match           93.7%;  Score 3454;  DB 5;  Length 501;
  Best Local Similarity  95.3%;  Pred. No. 1.88e-288;
  Matches   483;  Conservative    5;  Mismatches   9;  Indels  10;  Gaps   4;

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           |||| || |  |||:|| |||:    ||||| ||||||||||||||| ||||||||||
Qy       1 MEAAVAAPRPRLLLLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTE 60

Db      57 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGAVT--YCCNQDHCNKIELPTTGPFSEK 114
           ||||||||||||||||||||||||||||||:||  ||||||||||||||     |
Qy      61 TTDKVIHNSMCIAEIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIELPTT---V-K 116

Db     115 QSAGLGPVELAAVIAGPVCFVCIALMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 174
           |:||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Qy     117 SSPGLGPVELAAVIAGPVCFVCISLMLMVYICHNRTVIHHRVPNEEDPSLDRPFISEGTT 176

Db     175 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 234
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     177 LKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS 236

Db     235 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 294
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     237 REERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYT 296

Db     295 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 354
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     297 VTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV 356

Db     355 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 414
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     357 RHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCS 416

Db     415 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 474
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     417 IGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWY 476

Db     475 ANGAARLTALRIKKTLSQLSQQEGIKM 501
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Qy     477 ANGAARLTALRIKKTLSQLSQQEGIKM 503


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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 17, Application US/08149105.
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CC    Sequence 17, Application US/08149105
CC    Patent No. 5538892

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 8, Application PC/TUS9410080.
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CC    Sequence 8, Application PC/TUS9410080
CC     GENERAL INFORMATION:
CC       APPLICANT:  GENETICS INSTITUTE, INC.
CC       TITLE OF INVENTION:  RECEPTOR PROTEINS


RESULT    5
ID   US-08-149-105-15     STANDARD;     PRT;   501 AA.
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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 15, Application US/08149105.
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CC    Sequence 15, Application US/08149105
CC    Patent No. 5538892
  Query Match           67.3%;  Score 2481;  DB 5;  Length 501;
  Best Local Similarity  71.0%;  Pred. No. 5.17e-203;
  Matches   348;  Conservative   60;  Mismatches  67;  Indels  15;  Gaps  11;

Db      13 LVVLLLAGSGGSGP-RGIQALLCACTSCLQTNYTCETDGACMVSIFNLDGMEHHVRTCIP 71
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Qy      14 LLVLAAAAAAAAALLPGATALQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHNSMCIA 73

Db      72 KVELVPAGKPFYCL-SSE--DLRNTHCCYIDFCNKIDLRVPSGHLKRPEHPSMWGPVELV 128
            ::|:|  :|| |  ||    :  | ||  | ||||:|  |:  :| :  |:: |||||
Qy      74 EIDLIPRDRPFVCAPSSKTGSVTTTYCCNQDHCNKIEL--PTT-VKSS--PGL-GPVELA 127

Db     129 GIIAGPVFLLFLIIIIVFLVINYHQR-VYHNRQRLDMEDPSCEMC-LSKDKTLQDLVYDL 186
           ::|||||   |: | ::::|   | | | |:|   : |||| :   :|   || ||:||:
Qy     128 AVIAGPVC--FVCISLMLMVYICHNRTVIHHRVPNE-EDPSLDRPFISEGTTLKDLIYDM 184

Db     187 STSGSGSGLPLFVQRTVARTIVLQEIIGKGRFGEVWRGRWRGGDVAVKIFSSREERSWFR 246
           :||||||||||:||||:|||||||| ||||||||||||:||| :||||||||||||||||
Qy     185 TTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWFR 244

Db     247 EAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTIEGMIK 306
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Qy     245 EAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIK 304

Db     307 LALSAASGLAHLHMEIVGTQGKPGIAHRDLKSKNILVKKNGMCAIADLGLAVRHDAVTDT 366
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Qy     305 LALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDT 364

Db     367 IDIAPNQRVGTKRYMAPEVLDETINMKHFDSFKCADIYALGLVYWEIARRCNSGGVHEEY 426
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Qy     365 IDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDY 424

Db     427 QLPYYDLVPSDPSIEEMRKVVCDQKLRPNVPNWWQSYEALRVMGKMMRECWYANGAARLT 486
           |||||||||||||:||||||||:||||||:||:||| ||||||:|:|||||||||||||
Qy     425 QLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLT 484

Db     487 ALRIKKTLSQ 496
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Qy     485 ALRIKKTLSQ 494


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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 15, Application US/08317847.
XX
CC    Sequence 15, Application US/08317847
CC    Patent No. 5547854

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AC   xxxxxx
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DT   01-JAN-1900
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DE   Sequence 2, Application US/08341916.
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CC    Sequence 2, Application US/08341916
CC    Patent No. 5614609
CC     GENERAL INFORMATION:
CC       APPLICANT:  Ib  ez, Carlos F.
CC       APPLICANT:  Ryd n, Mikael
CC       APPLICANT:  J rnvall, Henrik
CC       TITLE OF INVENTION:  A No. 5614609el Serine Threonine Kinase Receptor
CC       NUMBER OF SEQUENCES:  6
CC       CORRESPONDENCE ADDRESS:
CC         ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
CC         STREET:  1100 New York Avenue, Suite 600
CC         CITY:  Washington
CC         STATE:  DC
CC         COUNTRY:  USA
CC         ZIP:  20005
CC       COMPUTER READABLE FORM:
CC         MEDIUM TYPE:  Floppy disk
CC         COMPUTER:  IBM PC compatible
CC         OPERATING SYSTEM:  PC-DOS/MS-DOS
CC         SOFTWARE:  PatentIn Release #1.0, Version #1.25
CC       CURRENT APPLICATION DATA:
CC         APPLICATION NUMBER:  US/08/341,916
CC         FILING DATE:  Herewith
CC         CLASSIFICATION:  514
CC       ATTORNEY/AGENT INFORMATION:
CC         NAME:  Goldstein, Jorge A.
CC         REGISTRATION NUMBER:  29,021
CC         REFERENCE/DOCKET NUMBER:  1459.0230001
CC       TELECOMMUNICATION INFORMATION:
CC         TELEPHONE:  (202)371-2600
CC         TELEFAX:  (202)371-2540
CC     INFORMATION FOR SEQ ID NO:  2:
CC       SEQUENCE CHARACTERISTICS:
CC         LENGTH:  493 amino acids
CC         TYPE:  amino acid
CC         TOPOLOGY:  linear
CC       MOLECULE TYPE:  protein
SQ   SEQUENCE   493 AA; 54800 MW; 1225231 CN;

  Query Match           64.7%;  Score 2384;  DB 6;  Length 493;
  Best Local Similarity  68.3%;  Pred. No. 1.63e-194;
  Matches   325;  Conservative   65;  Mismatches  76;  Indels  10;  Gaps   7;

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Qy      31 ATALQCFCHLCTKDNFTCVTDGLCFVSVTETTDKVIHNSMCIAEIDLIPRDRPFVCAPSS 90

Db      79 N--NVTKTECCFTDFCNNITLHLPTASPDAPRLGPTELTVVITVPVCLLSIAAMLTIWAC 136
           :  :|| | ||  | ||:|   |||:   :| ||| ||: ||: |||:: |: || :  |
Qy      91 KTGSVTTTYCCNQDHCNKI--ELPTTVKSSPGLGPVELAAVIAGPVCFVCISLMLMVYIC 148

Db     137 QDRQCTYRKTKRHNVEEPLAEYSLVNAGKTLKDLIYDATASGSGSGLPLLVQRTIARTIV 196
           ::|    ::   :: |:|  : :::: | |||||||| |:|||||||||||||||||||
Qy     149 HNRTVIHHRV-PNE-EDPSLDRPFISEGTTLKDLIYDMTTSGSGSGLPLLVQRTIARTIV 206

Db     197 LQEIVGKGRFGEVWHGRWCGEDVAVKIFSSRDERSWFREAEIYQTVMLRHENILGFIAAD 256
           ||| :|||||||||:|:| ||:|||||||||:|||||||||||||||||||||||||||||
Qy     207 LQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWFREAEIYQTVMLRHENILGFIAAD 266

Db     257 NKDNGTWTQLWLVSEYHEQGSLYDYLNRNIVTVAGMVKLALSIASGLAHLHMEIVGTQGK 316
           |||||||||||||:|||:|||:|||||  ||| ||:||||| |||||||||||||||||||
Qy     267 NKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIKLALSTASGLAHLHMEIVGTQGK 326

Db     317 PAIAHRDIKSKNILVKKCDTCAIADLGLAVKHDSIMNTIDIPQNPKVGTKRYMAPEMLDD 376
           |||||||:|||||||||  || ||||||||:|||  :||||: | :||||||||||:|||
Qy     327 PAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPNHRVGTKRYMAPEVLDD 386

Db     377 TMNVNIFESFKRADIYSVGLVYWEIARRCSVGGLVEEYQLPYYDMVPSDPSIEEMRKVVC 436
           ::|:: |||||||||::|||:|||||||||::|: |:|||||||:|||||||||||||||
Qy     387 SINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVC 446

Db     437 DQKLRPNLPNQWQSCEALRVMGRIMRECWYANGAARLTALRVKKTISQLCVKEDCK 492
           :||||||:||:|||||||::|||||||||||||||||:|||:|||   |  |
Qy     447 EQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQEGIK 502
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ALK-6

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MPsrch_nn   n.a. -  n.a. database search, using Smith-Waterman algorithm

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Description:     (1-1952) from US08436265.seq
Perfect Score:   1952
N.A. Sequence:        1 AAGCGGCGGCAGAAGTTGCC.........CCATTTTTTTATAAAAAAAA 1952
     Comp:              TTCGCCGCCGTCTTCAACGG.........GGTAAAAAAATATTTTTTTT

Scoring table:   TABLE default
                 Gap 6

Nmatch   STD :   Dbase 0;  Query 0

Searched:        333249 seqs, 555961234 bases x 2

[redacted] processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        embl-new11
                   1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2
                   9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
                   16.VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
                   23:VIR1 24:VIR2
Database:        genbank97
                   25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
                   32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
                   39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
                   46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1
                   53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
                   60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
                   67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
                   74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
                   80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
                   87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
                   94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9
Database:        genbank-new11
                   101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
                   107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
                   113:UNA 114:VRL
Database:        u-embl48_97
                   115:part1 116:part2

Statistics:      Mean 11.866;  Variance 4.400;  scale 2.697

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

Result          %
  No.  Score  Query  Length DB  ID          Description              Pred. No.
                Match
-----------------------------------------------------------------------------
    1   1944   99.6    1944 81  MMALK6A     M.musculus ALK-6 mRNA    0.00e+00
    2    933   47.8    2252 49  CHKRPK1     Chicken mRNA for rece    0.00e+00
    3    534   27.4    1599 87  RATRB4R1    Rat mRNA for bone mer    0.00e+00
    4    535   27.4    2620 20  S74037      bone morphogenetic pr    0.00e+00
    5    535   27.4    3003 20  RNRALK3     Rat mRNA for bone mor    0.00e+00
    6    535   27.4    3003 87  RATRALK3    Rat mRNA for bone mor    0.00e+00
    7    535   27.4    3167 88  S75359      bone morphogenetic pr    0.00e+00
    8    519   26.6    1599 81  MMALK3A     M.musculus ALK-3 mRNA    0.00e+00
    9    520   26.6    2292 84  MUSBMPRC    Mouse mRNA for BMP re    0.00e+00
   10    520   26.6    2402 82  MMU04672    Mus musculus type I r    0.00e+00

                              ALIGNMENTS

RESULT    1
LOCUS       MMALK6A      1944 bp    RNA             ROD       13-MAY-1994
DEFINITION  M.musculus ALK-6 mRNA, complete CDS.
ACCESSION   Z23143
NID         g437870
KEYWORDS    ALK-6 gene; serine/threonine kinase receptor.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Mus.
REFERENCE   1  (bases 1 to 1944)
  AUTHORS   ten Dijke,P., Yamashita,H., Ichijo,H., Franzen,P., Laiho,M.,
            Miyazono,K. and Heldin,C.H.
  TITLE     Characterization of type I receptors for transforming growth
            factor-beta and activin
  JOURNAL   Science 264 (5155), 101-104 (1994)
  MEDLINE   94188705
REFERENCE   2  (bases 1 to 1944)
  AUTHORS   Miyazono,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer
            Research, Biomedical, Center, Uppsala, S-751 24, Sweden
FEATURES             Location/Qualifiers
     source          1..1944
                     /organism="Mus musculus"
                     /strain="NIH Swiss"
                     /clone="ME-6"
                     /dev_stage="12 day embryo"
                     /clone_lib="cDNA library"
     CDS             187..1695
                     /codon_start=1
                     /product="ALK-6"
                     /db_xref="PID:g437871"
                     /db_xref="SWISS-PROT:P36898"
                     /translation="MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVN
                     NICSTDGYCFTMIEEDDSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNEC
                     NKDLHPTLPPLKDRDFVDGPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYS
                     IGLEQDETYIPPGESLRDLIEQSQSSSGSGSGLPLLVQRTIAKQIQMVKQIGKGPYGEV
                     WMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLY
                     LITDYHENGSLYDYLKSTTLDAKSMLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLK
                     SKNILVKKNGTCCIADLGLAVKFISDTNEVDIPPNTRVGTKRYMPPEVLDESLNRNHF
                     QSYIMADMYSFGLILWEIARRCVSGGIVEEYQLPYHDLVPSDPSYEDMREIVCMKKLR
                     PSFPNRWSSDECLRQMGKLMTECWAQNPASRLTALRVKKTLAKMSESQDIKL"
     sig_peptide     187..225
     mat_peptide     226..1692
                     /product="ALK-6"
BASE COUNT      546 a    446 c    503 g    449 t
ORIGIN

  Query Match           99.6%;  Score 1944;  DB 81;  Length 1944;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches  1944;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

RESULT    2
LOCUS       CHKRPK1      2252 bp    mRNA            VRT       28-DEC-1993
DEFINITION  Chicken mRNA for receptor protein kinase, complete cds.
ACCESSION   D13432
NID         g222862
KEYWORDS    TGF-beta receptor-related; receptor protein kinase;
            serine/threonine kinase; transmembrane protein.
SOURCE      Gallus gallus (library: lambda gt10) Stage 24-26 cDNA to mRNA,
            clone S1.
  ORGANISM  Gallus gallus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
            Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (sites)
  AUTHORS   Nohno,T.
  JOURNAL   Unpublished (1992)
```

REFERENCE 2 (bases 1 to 2252)
AUTHORS Sumitomo,S., Saito,T. and Nohno,T.
TITLE A new receptor protein kinase from chick embryo related to type II receptor for TGF-beta
JOURNAL DNA Sequence 3, 297-302 (1993)
MEDLINE 94003400
COMMENT Submitted (20-OCT-1992) to DDBJ by: Tsutomu Nohno
Department of Pharmacology
Kawasaki Medical School
577 Matsushima
Kurashiki 701-01
Japan
Phone: 086-462-1111

Query Match 47.8%; Score 933; DB 49; Length 2252;
Best Local Similarity 80.7%; Pred. No. 0.00e+00;
Matches 1227; Conservative 0; Mismatches 294; Indels 0; Gaps 0;

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 02:16:28 1997; MasPar time 188.32 Seconds
958.907 Million cell updates/sec

Tabular output not generated.

[redacted]: >US-08-436-265-17
Description: (1-1952) from US08436265.seq
Perfect Score: 1952
N.A. Sequence: 1 AAGCGGCGGCAGAAGTTGCC.....CCATTTTTTTATAAAAAAAA 1952
Comp: TTCGCCGCCGTCTTCAACGG.....GGTAAAAAAATATTTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 9.725; Variance 5.247; scale 1.853

[redacted] Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1952	100.0	1952	16	T06032	Mouse ALK-6 cDNA.	0.00e+00
2	1948	99.8	1952	11	Q66642	Mouse Activin recepto	0.00e+00
3	1662	85.1	2076	14	Q83531	Sequence encoding bon	0.00e+00
4	937	48.0	2252	20	T27229	Bone morphogenetic pr	0.00e+00
5	933	47.8	2252	23	T28022	Chick BMP type I rece	0.00e+00
6	533	27.3	1813	14	Q83530	Sequence encoding bon	0.00e+00
7	522	26.7	2070	11	Q66640	Mouse Activin recepto	0.00e+00
8	520	26.6	2402	20	T27228	Bone morphogenetic pr	0.00e+00
9	520	26.6	2402	14	Q90184	BRK-1 DNA.	0.00e+00
10	520	26.6	2402	23	T28021	Mouse BMP type I rece	0.00e+00

RESULT 1
ID T06032 standard; cDNA; 1952 BP.
AC T06032;
DT 13-FEB-1996 (first entry)
DE Mouse ALK-6 cDNA.
KW ALK-6; OP1 binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist; chimeric receptor; gene therapy; ss.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 187..1695
FT /*tag= a
FT sig_peptide 187..252
FT /*tag= b
FT mat_peptide 253..1692
FT /*tag= c
FT /product= mouse ALK-6
PN WO9530003-A2.
PD 09-NOV-1995.
PF 26-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.

RESULT 2
ID Q66642 standard; cDNA; 1952 BP.
AC Q66642;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 6 (mALK-6) cDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT 5'UTR 1..186
FT /*tag= a
FT /note= "contains an in-frame stop codon at
FT nucleotides 163-165"
FT CDS 187..1695
FT /*tag= b
FT /product= activin receptor-like kinase 6
FT 3'UTR 1696..1952
FT /*tag= c
FT /note= "there is no polyA signal indicating that
FT the cDNA was internally primed"
PN WO9411502-A.
PD 26-MAY-1994.
PF 17-NOV-1993; G02367.
PR 17-NOV-1992; GB-024057.
PR 08-MAR-1993; GB-004677.
PR 08-MAR-1993; GB-004680.
PR 28-MAY-1993; GB-011047.
PR 02-JUL-1993; GB-013763.
PR 03-AUG-1993; GB-016099.
PR 15-OCT-1993; GB-021344.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke P, Franzen P, Heldin C, Miyazono K, Yamashita H;
DR WPI; 94-183503/22.
DR P-PSDB; R55374.
Query Match 99.8%; Score 1948; DB 11; Length 1952;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 1950; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 3
ID Q83531 standard; DNA; 2076 BP.
AC Q83531;
DT 28-SEP-1995 (first entry)
DE Sequence encoding bone morphogenic protein receptor CFK1-43a.
KW Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW bone; cartilage; injury; treatment; inhibition; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 247..1755
FT /*tag= a

FT /product= Bone morphogenic protein receptor.
PN WO9507982-A.
PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR P-PSDB; R70238.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 2; Page 52-54; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence 2076 BP; 598 A; 481 C; 527 G; 470 T;

[redacted]y Match 85.1%; Score 1662; DB 14; Length 2076;
Best Local Similarity 94.7%; Pred. No. 0.0[illegible]0;
Matches 1776; Conservative 0; Mismatches 96; Indels 3; Gaps 3;

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Db   141 aacttcggctgaatcacaaccatttggcgctgagctatgacaagagagcaaacaaaaagt 200
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Qy    80 AACTTCGGCTGAATCACAACCATTTGGCGCTGAGCTATGACAAGAGAGCAAACAAAAAGT 139

Db   201 taaaggagcaactcggccataagtgac-agagaagttcgttgataacatgctcttacgaa 259
         |||||||||||| |||||||||||||  |||||||| ||||||||||||||||||||||
Qy   140 TAAAGGAGCAACCCGGCCATAAGTGAAGAGAGAAGTTTATTGATAACATGCTCTTACGAA 199

Db   260 gctctggaaaattaaatgtgggcaccaagaaggaggatggtgagagtacagcccccactg 319
         |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy   200 GCTCTGGAAAATTAAATGTGGGCACCAAGAAGGAGGATGGAGAGAGTACAGCCCCCACCC 259

Db   320 ctcggcccaaggtcctgcgttgtaaatgccaccaccactgtcctgaagactcagtcaaca 379
         |||||||||||| |||| |||||||||||||||||||||||| ||||||||||||||||
Qy   260 CTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCACTGTCCGGAAGACTCAGTCAACA 319

Db   380 atatctgcagcacagatgggtactgcttcacgatgatagaagaagacgactctggaacgc 439
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Qy   320 ATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGAATGC 379

Db   440 ctgttgtcacctccggatgcctaggactagaagggtcagattttcaatgtcgcgacacgc 499
         |||||||||||||| ||||| |||||||||||||||||||||||||||||||||| ||||| |
Qy   380 CTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGACACTC 439

Db   500 ccatccctcatcagagaaggtcaattgaatgctgcacagaaaggaacgaatgtaataaag 559
         |||| |||||||| ||||| |||||||||||||||||||||||||| || ||||||||||
Qy   440 CCATTCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAATAAAG 499

Db   560 atctccaccccacgctgcctcccctgaaggacagagattttgttgatggacccatacacc 619
         | |||||||||||| |||||||| || |||||||||||||||||||||| ||||||||||
Qy   500 ACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTTGATGGGCCCATACACC 559

Db   620 acaaagccttactcatatctgtgactgtctgtagtttactcttggtcctcattatttttat 679
         |||| ||||| || || |||||||||||||||||||||||||||||||||||||||||||
Qy   560 ACAAGGCCTTGCTTATCTCTGTGACTGTCTGTAGTTTACTCTTGGTCCTCATTATTTTAT 619

Db   680 tctgttacttcaggtataaaagacaagaagccagacctcggtacagcattgggctggagc 739
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Qy   620 TCTGTTACTTCAGGTATAAAAGACAAGAAGCCCGACCTCGGTACAGCATTGGGCTGGAGC 679

Db   740 aggatgaaacgtacattcctcctggagaatccctgagagacttgattgagcaatcgcaga 799
         |||| || || |||||||||||||||| |||||||||||||||| ||||| || ||||
Qy   680 AGGACGAGACATACATTCCTCCTGGAGAGTCCCTGAGAGACTTGATCGAGCAGTCTCAGA 739

Db   800 gctcgggaagtggctcaggactccctctgctggtccaaaggacaatagctaagcaaattc 859
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Qy   740 GCTCGGGAAGTGGATCAGGCCTCCCTCTGCTGGTCCAAAGGACAATAGCTAAGCAAATTC 799

Db   860 agatggtgaagcaaattggaaaaggtcgctatggcgaagtgtggatgggaaagtggcgtg 919
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Qy   800 AGATGGTGAAGCAGATTGGAAAAGGCCGCTATGGCGAGGTGTGGATGGGAAAGTGGCGTG 859

Db   920 gagaaaaggtagctgtgaaagtgttcttcaccacggaggaagccagctggttccgagaga 979
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Qy   860 GAGAAAAGGTGGCTGTGAAAGTGTTCTTCACCACGGAGGAAGCCAGCTGGTTCCGAGAGA 919

Db   980 ctgagatatatcagacggtcctgatgaggcacgagaacattctgggggttcattgcagcag 1039
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Qy   920 CTGAGATATATCAGACGGTCCTGATGCGGCATGAGAATATTCTGGGGTTCATTGCTGCAG 979

Db  1040 atatcaaagggactgggtcttggactcagttatacctcatcacagactatcatgaaaacg 1099
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Qy   980 ATATCAAAGGGACTGGGTCCTGGACTCAGTTGTACCTCATCACAGACTATCATGAAAACG 1039

Db  1100 ggtctctttatgactatctgaaatccaccaccttagatgccaagtccatgctgaagctag 1159
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Qy  1040 GCTCCCTTTATGACTATCTGAAATCCACCACCTTAGACGCAAAGTCCATGCTGAAGCTAG 1099

Db  1160 cctactcgtctgtcagcggcctgtgccatctacacacggaaatcttcagcactcaaggca 1219
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Qy  1100 CCTACTCCTCTGTCAGCGGCCTATGCCATTTACACACGGAAATCTTTAGCACTCAAGGCA 1159

Db  1220 agccagccattgcccatcgggacttgaaaagtaaaaacatcctggtgaagaaaaatggaa 1279
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Qy  1160 AGCCAGCAATCGCCCATCGAGACTTG-AAAAGTAAAACATCCTGGTGAAGAAAAATGGAA 1219

Db  1280 cttgctgcatagcagacctgggcctggctgtcaagttcattagtgacacaaatgaggttg 1339
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Qy  1220 CTTGCTGCATAGCAGACCTGGGCTTGGCTGTCAAGTTCATTAGTGACACAAATGAGGTTG 1279

Db  1340 acattccacccaacacccgggttggcaccaagcgctatatgcctccagaagtgctggacg 1399
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Qy  1280 ACATCCCACCCAACACCCGGGTTGGCACCAAGCGCTATATGCCTCCAGAAGTGCTGGACG 1339

Db  1400 agagcttgaatagaactcatttccagtcctacatcatggctgacatgtacagctttggac 1459
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Qy  1340 AGAGCTTGAATAGAAACCATTTCCAGTCCTACATTATGGCTGACATGTACAGCTTTGGAC 1399

Db  1460 tcatcctctgggagattgcaaggagatgtgtttctggaggtatagtggaagaataccagc 1519
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Qy  1400 TCATCCTCTGGGAGATTGCAAGGAGATGTGTTTCTGGAGGTATAGTGGAAGAATACCAGC 1459

Db  1520 ttccatatcacgacctggtgcccagtgacccctcttatgaggacatgagagaaattgtgt 1579
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Qy  1460 TTCCCTATCACGACCTGGTGCCCAGTGACCCTTCTTATGAGGACATGAGAGAAATTGTGT 1519

Db  1580 gtatgaagaagttacggccttcattccccaatcgatggagcagtgacgagtgcctcaggc 1639
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Qy  1520 GCATGAAGAAGTTACGGCCTTCATTCCCCAATCGATGGAGCAGTGATGAGTGTCTCAGGC 1579

Db  1640 aaatggggaagcttatgacagagtgctgggcgcataatcctgcctccaggctgacggccc 1699
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Qy  1580 AGATGGGGAAGCTTATGACAGAGTGCTGGGCGCAGAATCCTGCCTCCAGGCTGACGGCCC 1639

Db  1700 tgagagttaagaaaacacttgccaaaatgtcagagtcccaggacattaaactctgacgtc 1759
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Qy  1640 TGAGAGTTAAGAAAACCCTTGCCAAAATGTCAGAGTCCCAGGACATTAAACTCTGACGTC 1699

Db  1760 aggtacttgtggacagagcaagcaattacacagaagcatccttagcccaagccttgaacg 1819
         || |||||||||||||||||| |||| |||||||||| |||||||||||||||||||||||
Qy  1700 AGATACTTGTGGACAGAGCAAG-AATTTCACAGAAGCATCGTTAGCCCAAGCCTTGAACG 1758

Db  1820 ttcatctactgcccagtgagttcagactttcctctaagagagcaagctggacagacacag 1879
         ||  |||||||||||||||||| |||||||||| | ||| |||||||||||||||||||
Qy  1759 TTAGCCTACTGCCCAGTGAGTTCAGACTTTCCTGGAAGAGAGCACGGTGGGCAGACACAG 1818
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Db    1880 aggaacccagaaacacggcttcaccatggctttctgaggaggggaaaccatttgggtaac 1939
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Qy    1819 AGGAACCCAGAAACACGGATTCATCATGGCTTTCTGAGGAGGAGAAACTGTTTGGGTAAC 1878

Db    1940 ttgttcaagatatgatgcatgttcctttctaagaaagccctgtatttttgggattaccatt 1999
           |||||||||||||||||||||| |||||||||||||||||||||||||  |||||||||
Qy    1879 TTGTTCAAGATATGATGCATGTTGCTTTCTAAGAAAGCCCTGTATTTTGA-ATTACCATT 1937

Db    2000 ttttttaaagaagaa 2014
           |||||  || || ||
Qy    1938 TTTTTATAAAAAAAA 1952
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 02:25:10 1997; MasPar time 1244.32 Seconds
1005.627 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-17
Description: (1-1952) from US08436265.seq
Perfect Score: 1952
N.A. Sequence: 1 AAGCGGCGGCAGAAGTTGCC.....CCATTTTTTTATAAAAAAAA 1952
Comp: TTCGCCGCCGTCTTCAACGG.....GGTAAAAAAATATTTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description	Pred. No.
1	295	15.1	471	164	W34981	mc33h08.r1 Soares mou	0.00e+00
2	200	10.2	404	165	W39552	zc18g04.r1 Soares par	0.00e+00
3	144	7.4	739	231	HSA53838	zf53c07.r1 Soares ret	4.23e-275
4	144	7.4	739	10	AA053838	zf53c07.r1 Soares ret	4.23e-275
5	132	6.8	259	38	H33315	EST109182 Rattus sp.	2.26e-245
6	126	6.5	515	43	C17679	Human placenta cDNA 5	1.33e-230
7	126	6.5	515	239	HSC6799	Human placenta cDNA 5	1.33e-230
8	122	6.2	631	168	W48139	mc85f09.r1 Soares mou	8.53e-221
9	93	4.8	354	63	HSC1TF041	H. sapiens partial cD	7.43e-151
10	92	4.7	343	103	R20290	yg20f06.r1 Homo sapie	1.73e-148

c ALIGNMENTS

RESULT 1
LOCUS W34981 471 bp mRNA EST 11-SEP-1996
DEFINITION mc33h08.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 350367 5' similar to gb:Z22535_cds1 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (HUMAN); gb:Z23143 M.musculus ALK-6 mRNA, complete CDS (MOUSE);.
ACCESSION W34981
NID g1316900
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 471)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:222167
Seq primer: ETPrimer
High quality sequence stop: 324.
FEATURES Location/Qualifiers
source 1..471
/organism="Mus musculus"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
/clone="350367"
/clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
mRNA <1..>471
BASE COUNT 135 a 115 c 116 g 104 t 1 others
ORIGIN

Query Match 15.1%; Score 295; DB 164; Length 471;
Best Local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 346; Conservative 0; Mismatches 4; Indels 8; Gaps 8;

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat May 24 07:07:33 1997; MasPar time 66.71 Seconds
836.429 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-17
Description: (1-1952) from US08436265.seq
Perfect Score: 1952
N.A. Sequence: 1 AAGCGGCGGCAGAAGTTGCC.....CCATTTTTTTATAAAAAAAA 1952
Comp: TTCGCCGCCGTCTTCAACGG.....GGTAAAAAAATATTTTTTTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 53119 seqs, 14293498 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 9.244; Variance 4.492; scale 2.058

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1952	100.0	1952	11	PCT-US95-0	Sequence 7, Applicatio	0.00e+00
2	1664	85.2	2076	10	PCT-US94-1	Sequence 3, Applicatio	0.00e+00
3	533	27.3	1813	10	PCT-US94-1	Sequence 1, Applicatio	0.00e+00
4	508	26.0	2932	11	PCT-US95-0	Sequence 5, Applicatio	0.00e+00
5	263	13.5	1647	10	PCT-US94-1	Sequence 7, Applicatio	2.72e-197
6	252	12.4	1794	10	PCT-US94-1	Sequence 9, Applicatio	1.99e-196
7	252	12.9	1506	5	US-08-317-	Sequence 4, Applicatio	8.55e-188
8	252	12.9	1506	5	US-08-317-	Sequence 2, Applicatio	8.55e-188
9	252	12.9	1506	5	US-08-149-	Sequence 2, Applicatio	8.55e-188
10	252	12.9	1506	5	US-08-149-	Sequence 4, Applicatio	8.55e-188

ALIGNMENTS

RESULT 1
ID PCT-US95-05467-7 STANDARD; DNA; UNC; 1952 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 7, Application PC/TUS9505467.
CC Sequence 7, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-[illegible] CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
CC NUMBER OF SEQUENCES: 15

RESULT 2
ID PCT-US94-10080-3 STANDARD; DNA; UNC; 2076 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 3, Application PC/TUS9410080.
CC Sequence 3, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genetics Institute Inc.- Legal Affairs
CC STREET: 87 CambridgePark Drive
Query Match 85.2%; Score 1664; DB 10; Length 2076;
Best Local Similarity 94.8%; Pred. No. 0.00e+00;
Matches 1777; Conservative 0; Mismatches 95; Indels 3; Gaps 3;

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Db    141 AACTTCGGCTGAATCACAACCATTTGGCGCTGAGCTATGACAAGAGAGCAAACAAAAAGT 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     80 AACTTCGGCTGAATCACAACCATTTGGCGCTGAGCTATGACAAGAGAGCAAACAAAAAGT 139

Db    201 TAAAGGAGCAACTCGGCCATAAGTGAC-AGAGAAGTTCGTTGATAACATGCTCTTACGAA 259
          |||||||||||| |||||||||||||  ||||||||  ||||||||||||||||||||||
Qy    140 TAAAGGAGCAACCCGGCCATAAGTGAAGAGAGAAGTTTATTGATAACATGCTCTTACGAA 199

Db    260 GCTCTGGAAAATTAAATGTGGGCACCAAGAAGGAGGATGGTGAGAGTACAGCCCCCACTG 319
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Qy    200 GCTCTGGAAAATTAAATGTGGGCACCAAGAAGGAGGATGGAGAGAGTACAGCCCCCACCC 259

Db    320 CTCGGCCCAAGGTCCTGCGTTGTAAATGCCACCACCACTGTCCTGAAGACTCAGTCAACA 379
          |||||||||||| |||| |||||||||||||||||||||||| ||||||||||||||||
Qy    260 CTCGGCCCAAGATCCTACGTTGTAAATGCCACCACCACTGTCCGGAAGACTCAGTCAACA 319

Db    380 ATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGACGACTCTGGAACGC 439
          |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Qy    320 ATATCTGCAGCACAGATGGGTACTGCTTCACGATGATAGAAGAAGATGACTCTGGAATGC 379

Db    440 CTGTTGTCACCTCCGGATGCCTAGGACTAGAAGGGTCAGATTTTCAATGTCGCGACACGC 499
          |||||||||||||| ||||| |||||||||||||||||||||||||||||||||| ||||| |
Qy    380 CTGTTGTCACCTCTGGATGTCTAGGACTAGAAGGGTCAGATTTTCAATGTCGTGACACTC 439

Db    500 CCATCCCTCATCAGAGAAGGTCAATTGAATGCTGCACAGAAAGGAACGAATGTAATAAAG 559
          |||| |||||||| ||||| |||||||||||||||||||||||||| || ||||||||||
Qy    440 CCATTCCTCATCAAAGAAGATCAATTGAATGCTGCACAGAAAGGAATGAGTGTAATAAAG 499

Db    560 ATCTCCACCCCACGCTGCCTCCCCTGAAGGACAGAGATTTTGTTGATGGACCCATACACC 619
          | |||||||||| |||||||| || |||||||||||||||||||||||| ||||||||||
Qy    500 ACCTCCACCCCACTCTGCCTCCTCTCAAGGACAGAGATTTTGTTGATGGGCCCATACACC 559

Db    620 ACAAAGCCTTACTCATATCTGTGACTGTCTGTAGTTTACTCTTGGTCCTCATTATTTTAT 679
          |||| ||||| || || ||||||||||||||||||||||||||||||||||||||||||||
Qy    560 ACAAGGCCTTGCTTATCTCTGTGACTGTCTGTAGTTTACTCTTGGTCCTCATTATTTTAT 619

Db    680 TCTGTTACTTCAGGTATAAAAGACAAGAAGCCAGACCTCGGTACAGCATTGGGCTGGAGC 739
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Qy    620 TCTGTTACTTCAGGTATAAAAGACAAGAAGCCCGACCTCGGTACAGCATTGGGCTGGAGC 679

Db    740 AGGATGAAACGTACATTCCTCCTGGAGAATCCCTGAGAGACTTGATTGAGCAATCGCAGA 799
          |||| || || |||||||||||||||| |||||||||||||||| |||| || ||||||||
Qy    680 AGGACGAGACATACATTCCTCCTGGAGAGTCCCTGAGAGACTTGATCGAGCAGTCTCAGA 739

Db    800 GCTCGGGAAGTGGCTCAGGACTCCCTCTGCTGGTCCAAAGGACAATAGCTAAGCAAATTC 859
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Qy    740 GCTCGGGAAGTGGATCAGGCCTCCCTCTGCTGGTCCAAAGGACAATAGCTAAGCAAATTC 799

Db    860 AGATGGTGAAGCAAATTGGAAAAGGTCGCTATGGCGAAGTGTGGATGGGAAAGTGGCGTG 919
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Qy    800 AGATGGTGAAGCAGATTGGAAAAGGCCGCTATGGCGAAGTGGATGGGAAAGTGGCGTG 859

Db    920 GAGAAAAGGTAGCTGTGAAAGTGTTCTTCACCACGGAGGAAGCCAGCTGGTTCCGAGAGA 979
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy    860 GAGAAAAGGTGGCTGTGAAAGTGTTCTTCACCACGGAGGAAGCCAGCTGGTTCCGAGAGA 919

Db    980 CTGAGATATATCAGACGGTCCTGATGAGGCACGAGAACATTCTGGGGTTCATTGCAGCAG 1039
          |||||||||||||||||||||||||| |||| ||||| |||||||||||||||| ||||
Qy    920 CTGAGATATATCAGACGGTCCTGATGCGGCATGAGAATATTCTGGGGTTCATTGCTGCAG 979

Db   1040 ATATCAAAGGGACTGGGTCTTGGACTCAGTTATACCTCATCACAGACTATCATGAAAACG 1099
          |||||||||||||||||| |||||||||| |||||||||||||||||||||||||||||
Qy    980 ATATCAAAGGGACTGGGTCCTGGACTCAGTTGTACCTCATCACAGACTATCATGAAAACG 1039

Db   1100 GGTCTCTTTATGACTATCTGAAATCCACCACCTTAGATGCCAAGTCCATGCTGAAGCTAG 1159
          | || |||||||||||||||||||||||||||||| || ||||||||||||||||||||
Qy   1040 GCTCCCTTTATGACTATCTGAAATCCACCACCTTAGACGCAAAGTCCATGCTGAAGCTAG 1099

Db   1160 CCTACTCGTCTGTCAGCGGCCTGTGCCATCTACACACGGAAATCTTCAGCACTCAAGGCA 1219
          ||||||| |||||||||||||| |||||| |||||||||||||||| ||||||||||||
Qy   1100 CCTACTCCTCTGTCAGCGGCCTATGCCATTTACACACGGAAATCTTTAGCACTCAAGGCA 1159

Db   1220 AGCCAGCCATTGCCCATCGGGACTTGAAAAGTAAAAACATCCTGGTGAAGAAAAATGGAA 1279
          ||||||| || |||||||| |||||||||||||||||||||||||||||||||||||||
Qy   1160 AGCCAGCAATCGCCCATCGAGACTTGAAAAGTAAAAACATCCTGGTGAAGAAAAATGGAA 1219

Db   1280 CTTGCTGCATAGCAGACCTGGGCCTGGCTGTCAAGTTCATTAGTGACACAAATGAGGTTG 1339
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Qy   1220 CTTGCTGCATAGCAGACCTGGGCTTGGCTGTCAAGTTCATTAGTGACACAAATGAGGTTG 1279

Db   1340 ACATTCCACCCAACACCCGGGTTGGCACCAAGCGCTATATGCCTCCAGAAGTGCTGGACG 1399
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1280 ACATCCCACCCAACACCCGGGTTGGCACCAAGCGCTATATGCCTCCAGAAGTGCTGGACG 1339

Db   1400 AGAGCTTGAATAGAACTCATTTCCAGTCCTACATCATGGCTGACATGTACAGCTTTGGAC 1459
          |||||||||||||| |||||||||||||||| |||||||||||||||||||||||||||
Qy   1340 AGAGCTTGAATAGAAACCATTTCCAGTCCTACATTATGGCTGACATGTACAGCTTTGGAC 1399

Db   1460 TCATCCTCTGGGAGATTGCAAGGAGATGTGTTTCTGGAGGTATAGTGGAAGAATACCAGC 1519
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1400 TCATCCTCTGGGAGATTGCAAGGAGATGTGTTTCTGGAGGTATAGTGGAAGAATACCAGC 1459
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Db    1520 TTCCATATCACGACCTGGTGCCCAGTGACCCCTCTTATGAGGACATGAGAGAAATTGTGT 1579
           |||| |||||||||||||||||||||||| |||||||||||||||||||||||||||||
Qy    1460 TTCCCTATCACGACCTGGTGCCCAGTGACCCTTCTTATGAGGACATGAGAGAAATTGTGT 1519

Db    1580 GTATGAAGAAGTTACGGCCTTCATTCCCCAATCGATGGAGCAGTGACGAGTGCCTCAGGC 1639
           | |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||
Qy    1520 GCATGAAGAAGTTACGGCCTTCATTCCCCAATCGATGGAGCAGTGATGAGTGTCTCAGGC 1579

Db    1640 AAATGGGGAAGCTTATGACAGAGTGCTGGGCGCATAATCCTGCCTCCAGGCTGACGGCCC 1699
           | |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Qy    1580 AGATGGGGAAGCTTATGACAGAGTGCTGGGCGCAGAATCCTGCCTCCAGGCTGACGGCCC 1639

Db    1700 TGAGAGTTAAGAAAACACTTGCCAAAATGTCAGAGTCCCAGGACATTAAACTCTGACGTC 1759
           |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Qy    1640 TGAGAGTTAAGAAAACCCTTGCCAAAATGTCAGAGTCCCAGGACATTAAACTCTGACGTC 1699

Db    1760 AGGTACTTGTGGACAGAGCAAGGAATTACACAGAAGCATCCTTAGCCCAAGCCTTGAACG 1819
           || |||||||||||||||||| |||| |||||||||||| ||||||||||||||||||||
Qy    1700 AGATACTTGTGGACAGAGCAAG-AATTTCACAGAAGCATCGTTAGCCCAAGCCTTGAACG 1758

Db    1820 TTGATCTACTGCCCAGTGAGTTCAGACTTTCCTCTAAGAGAGCAAGCTGGACAGACACAG 1879
           ||   |||||||||||||||||||||||||||||  ||||||||| ||| |||||||||
Qy    1759 TTAGCCTACTGCCCAGTGAGTTCAGACTTTCCTGGAAGAGAGCACGGTGGGCAGACACAG 1818

Db    1880 AGGAACCCAGAAACACGGCTTCACCATGGCTTTCTGAGGAGGGGAAACCATTTGGGTAAC 1939
           |||||||||||||||||| |||| |||||||||||||||| |||| | ||| |||||||||
Qy    1819 AGGAACCCAGAAACACGGATTCATCATGGCTTTCTGAGGAGGAGAAACTGTTTGGGTAAC 1878

Db    1940 TTGTTCAAGATATGATGCATGTTGCTTTCTAAGAAAGCCCTGTATTTTGGGATTACCATT 1999
           ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Qy    1879 TTGTTCAAGATATGATGCATGTTGCTTTCTAAGAAAGCCCTGTATTTTGGA-TTACCATT 1937

Db    2000 TTTTTTAAAGAAGAA 2014
           |||||  || || ||
Qy    1938 TTTTTATAAAAAAAA 1952

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:       Tue Jun 24 17:57:04 1997;  MasPar time 10.43 Seconds
                                         524.426 Million cell updates/sec
Tabular output not generated.

Title:          >US-08-436-265-18
Description:    (1-502) from US08436265.pep
Perfect Score:  3740
Sequence:       1 MLLRSSGKLNVGTKKEDGES.........TALRVKKTLAKMSESQDIKL 502

Scoring table:  PAM 150
                Gap 11

Searched:       92623 seqs, 10896596 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:       a-geneseq26
                  1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                  8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                  14:part14 15:part15 16:part16 17:part17 18:part18
                  19:part19

Statistics:     Mean 35.960;  Variance 153.657;  scale 0.234

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

                    %
Result              Query
  No.  Score        Match Length DB  ID          Description                Pred. No.
```

```
 ---------------------------------------------------------------------------
    1   3740  100.0    502 14  R85209      Mouse ALK-6.               0.00e+00
    2   3728   99.7    502 10  R55374      Mouse Activin recepto      0.00e+00
    3   3711   99.2    502 13  R70238      Bone morphogenic prot      0.00e+00
    4   3466   92.7    502 19  R95226      Chick BMP type I rece      0.00e+00
    5   3466   92.7    502 17  R96202      Bone morphogenetic pr      0.00e+00
    6   2757   73.7    532 14  R85207      Human ALK-3.               3.32e-259
    7   2757   73.7    532 10  R55368      Human Activin recepto      3.32e-259
    8   2756   73.7    532 19  R95225      Mouse BMP type I rece      4.18e-259
    9   2756   73.7    532 17  R96201      Bone morphogenetic pr      4.18e-259
   10   2756   73.7    532 13  R74343      BRK-1 protein.             4.18e-259
                    ALIGNMENTS

RESULT    1
ID   R85209 standard; Protein; 502 AA.
AC   R85209;
DT   13-FEB-1996  (first entry)
DE   Mouse ALK-6.
KW   ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;
KW   morphogen; agonist; antagonist.
OS   Mus sp.
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT   /label= Sig_peptide
FT   Domain          23..122
FT   /label= Intracellular_domain
FT   Domain          123..205
FT   /label= Transmembrane_domain
FT   Domain          206..497
FT   /label= Intracellular_domain
FT   /note= "serine/threonine-kinase domain"
PN   WO9530003-A2.
PD   09-NOV-1995.
PF   28-APR-1995; U05467.
PR   29-APR-1994; US-236428.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Dijke PT,  Heldin C,  Miyazano K,  Sampath KT;

RESULT    2
ID   R55374 standard; Protein; 502 AA.
AC   R55374;
DT   20-JAN-1995  (first entry)
DE   Mouse Activin receptor-like kinase 6 (mALK-6).
KW   serine threonine kinases; activin receptors; Act-R; superfamily;
KW   transforming growth factor; TGF; diagnostics; detection; therapy;
KW   rheumatoid arthritis; glomerular nephritis; fibrosis.
OS   Mus musculus.
PN   WO9411502-A.
PD   26-MAY-1994.
PF   17-NOV-1993; G02367.
PR   17-NOV-1992; GB-024057.
PR   08-MAR-1993; GB-004677.
PR   08-MAR-1993; GB-004680.
PR   28-MAY-1993; GB-011047.
PR   02-JUL-1993; GB-013763.
PR   03-AUG-1993; GB-016099.
PR   15-OCT-1993; GB-021344.
PA   (LUDW-) LUDWIG INST CANCER RES.
PI   Dijke P,  Franzen P,  Heldin C,  Miyazono K,  Yamashita H;
DR   WPI; 94-183503/22.

RESULT    3
ID   R70238 standard; Protein; 502 AA.
AC   R70238;
DT   28-SEP-1995  (first entry)
DE   Bone morphogenic protein receptor CFK1-43a.
KW   Bone morphogenic protein; receptor; serine/threonine kinase; BMP;
KW   bone; cartilage; injury; treatment; inhibition.
OS   Rattus rattus.
PN   WO9507982-A.
```

PD 23-MAR-1995.
PF 07-SEP-1994; U10080.
PR 17-SEP-1993; US-123934.
PA (GEMY) GENETICS INST INC.
PI Celeste AJ, Thies RS, Wozney JM, Yamaji N;
DR WPI; 95-131350/17.
DR N-PSDB; Q83531.
PT Truncated BMP and serine/threonine kinase receptor proteins -
PT used to inhibit the effects of BMP-2 and/or BMP-4.
PS Claim 17; Page 54-55; 83pp; English.
CC Truncated bone morphogenic protein (BMP) receptors and
CC serine/threonine kinase receptors may be used in compositions to
CC inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated
CC receptors pref. comprise the ligand binding domain, but not the
CC serine/threonine kinase and transmembrane domains. The truncated
CC proteins are soluble and will be excreted into supernatant by
CC recombinant mammalian cells expressing them. Such cells can be
CC delivered in a medium or matrix which partially impedes their
CC mobility, thereby localising the cells to a site of bone or
CC cartilage injury.
SQ Sequence [illegible] AA;

Query Match 99.2%; Score 3711; DB 13; Length 502;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Db      1 mllrssgklnvgtkkedgestaptarpkvlrckchhhcpedsvnnicstdgycftmieed 60
          |||||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||||
Qy      1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db     61 dsgtpvtvnlegsdfqcrdtpiphqrrsieccternecnkdlhptlppqlkdrdfvd 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db    121 gpihhkallisvtvcslllvliilfcyfrykrqearprysigleqdetyippgeslrdli 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db    181 eqsqsssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db    241 wfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldaks 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db    301 mlklayssvsglchlhteifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db    361 tnevdippntrvgtkrymppevldeslnrthfqsyimadmysfglilweiarrcvsggiv 420
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Qy    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db    421 eeyqlpyhdlvpsdpsyedmreivcmkklrpsfpnrwssdeclrqmgklmtecwahnpas 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Qy    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db    481 rltalrvkktlakmsesqdikl 502
          |||||||||||||||||||||||
Qy    481 RLTALRVKKTLAKMSESQDIKL 502
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RESULT 4
ID R95226 standard; Protein; 502 AA.
AC R95226;
DT 31-DEC-1996 (first entry)
DE Chick BMP type I receptor kinase protein (BRK-2).
KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;
KW BMP type I receptor kinase; BRK-2; BMP receptor.
OS Gallus sp.

PN WO9614579-A1.
PD 17-MAY-1996.
PF 30-OCT-1995; U14027.
PR 04-NOV-1994; US-334178.
PR 05-JUN-1995; US-462467.
PA (PROC) PROCTER & GAMBLE CO.
PI Rosenbaum JS;
DR WPI; 96-251887/25.
DR N-PSDB; T28022.
PT Assays for bone morphogenetic protein activities - using complex of
PT BMP type I receptor kinase protein and BMP receptor kinase protein
PT BRK-3
PS Claim 2; Page 70-71; 101pp; English.
CC Full-length chick bone morphogenetic protein (BMP) type I receptor
CC kinase protein-2 (BRK-2) (R95226) is a receptor capable of binding
CC BMP and transducing a signal initiated by the binding. Its amino
CC acid sequence was deduced from a cDNA clone (T28022). A BMP
CC receptor kinase protein complex formed of full-length, incomplete
CC or soluble BMP type I receptor kinase protein and full-length,
CC incomplete or soluble BMP type II receptor kinase-3 (BRK-3) (see
CC also R95222-25 and R95227-34) is useful for screening cpds. for BMP
CC receptor affinity or for determining the concentration of a BMP
CC receptor ligand in a clinical sample. The complex can be expressed
CC by host cells co-transfected with vectors carrying the appropriate
CC DNA sequences (see also T28018-30).
SQ Sequence 502 AA;

Query Match 92.7%; Score 3466; DB 19; Length 502;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

```
Db      1 mpllssskslmesrkedsegtapappqkklscqchhhcpedsvnstcstdgycftiieed 60
          | | ||:||:: ::|||:|:|||:|  | | | ||||||||||: ||||||||:||||
Qy      1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db     61 dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlhptlpplknrdfae 120
          |||  :|| ||||||||||||||||||||||||| :: ||| |||||||||:||| :
Qy     61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db    121 gnihhkallisvtvcsillvliiifcyfrykrqearprysigleqdetyippgeslkdli 180
          | ||||||||||||:||||:|||||||||||||||||||||||||||||||||||:|||
Qy    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db    181 eqsqsssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db    241 wfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldtkg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:
Qy    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db    301 mlklayssvsglchlhtgifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db    361 tnevdippntrvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiv 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db    421 eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas 480
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Qy    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db    481 rltalrvkktlakmsesqdikl 502
          |||||||||||||||||||||||
Qy    481 RLTALRVKKTLAKMSESQDIKL 502
```

RESULT 5
ID R96202 standard; Protein; 502 AA.
AC R96202;

DT 22-AUG-1996 (first entry)
DE Bone morphogenetic protein type-I receptor kinase-2.
KW Chicken; bone morphogenetic protein receptor kinase-2;
KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;
KW bone disorder; osteogenic; bone morphogenetic protein-agonist;
KW drug screening; reporter gene; bone morphogenetic protein-antagonist;
KW hormone-responsive element.
OS Gallus domesticus.
FH Key Location/Qualifiers
FT Peptide 186..191
FT /note= "Conserved BRK-2 motif"
PN WO9614412-A2.
PD 17-MAY-1996.
PF 30-OCT-1995; U14085.
PR 04-NOV-1994; US-[illegible]1179.
PA (PROC) PROCTER & GAMBLE CO.
PI Nohno T, Rosenbaum JS;
DR WPI; 96-251762/25.
DR N-PSDB; T27229.
PT Isolated bone morphogenic protein receptor kinase protein - used to
PT determine if a test cpd. is capable of binding to, or is
PT (ant)agonist of BMP receptor kinase protein transcription
PS Example 4; Page 67-68; 87pp; English.
CC The sequence represents chicken bone morphogenetic protein (BMP)
CC receptor type-I kinase-2 (BRK-1), which induces cellular
CC differentiation in response to BMP. Complex formation between
CC BRK-2 and type-II BRK-3 may be studied by co-expression of both
CC genes, followed by screening with an antibody generated against an
CC intracellular kinase peptide sequence present in BRK-1. BRK-2
CC contains an SGSGSG motif in the juxtamembrane region, 35-40 amino
CC acids from the transmembrane region, and the C-terminus region is
CC very short. The extracellular domain contains a cluster of
CC cysteine residues (cysteine box) within 25-30 amino acids of the
CC trnasmembrane region, and an upstream cysteine box after the
CC putative signal peptide. The BRK-3 receptor and antibodies against
CC it may be used in diagnostic assays for BMP disorders, or in
CC therapy to bind or scavenge BMPs. In addition, expression of the
CC BRK-3 gene along with a reporter gene under the control of a
CC hormone- responsive element in a cell culture may be used to screen
CC compounds for BRK-agonist or -antagonist activity, by monitoring
CC reporter gene expression.
SQ Sequence 502 AA;

Query Match 92.7%; Score 3466; DB 17; Length 502;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

```
Db     1 mpllssskslsmesrkedsegtapappqkklscqchhhcpedsvnstcstdgycftiieed 60
         | | ||:||:: ::|||:|:|||:|  | | | |||||||||||: ||||||||:||||
Qy     1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db    61 dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlhptlpplknrdfae 120
         |||  :|| |||||||||||||||||||||||||| :: ||| |||||||||:||| :
Qy    61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db   121 gnihhkallisvtvcsillvliiifcyfrykrqearprysigleqdetyippgeslkdli 180
         | |||||||||||||:||||||:|||||||||||||||||||||||||||||||||:|||
Qy   121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db   181 eqsqsssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:
Qy   181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db   241 wfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldtkg 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:
Qy   241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db   301 mlklayssvsglchlhtgifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360
         |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy   301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db   361 tnevdippntrvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiv 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db   421 eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas 480
         |||||||||||||||||||||||:|:|||||||||||||||||||| ||||:||||
Qy   421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db   481 rltalrvkktlakmsesqdikl 502
         |||||||||||||||||||||
Qy   481 RLTALRVKKTLAKMSESQDIKL 502
```

RESULT 6
ID R85207 standard; Protein; 532 AA.
AC R85207;
DT 13-FEB-1996 (first entry)
DE Human ALK-3.
KW ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;
KW morphogen; agonist; antagonist.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Sig_peptide
FT Domain 24..152
FT /label= Extracellular_domain
FT Domain 153..235
FT /label= Transmembrane_domain
FT Domain 236..527
FT /label= Intracellular_domain
FT /note= "serine/threonine-kinase domain"
PN WO9[illegible] A2.
PD 09-NOV-1995.
PF 28-APR-1995; U05467.
PR 29-APR-1994; US-236428.
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (LUDW-) LUDWIG INST CANCER RES.
PI Dijke PT, Heldin C, Miyazano K, Sampath KT;
DR WPI; 95-393076/50.
DR N-PSDB; T06031.
PT Identifying osteogenic protein-1 receptor-binding analogue - useful
PT in the design of morphogen agonists and antagonists for therapeutic,
PT diagnostic and experimental purposes
PS Claim 1; Page 68-71; 95pp; English.
CC The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given in
CC R85206, R85207 and R85209) have specific binding affinity for
CC osteogenic protein 1 (OP1) and OP1-related analogues. The
CC receptors are used to identify novel morphogen receptor binding
CC analogues useful in drug design.
SQ Sequence 532 AA;

Query Match 73.7%; Score 2757; DB 14; Length 532;
Best Local Similarity 71.9%; Pred. No. 3.32e-259;
Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;

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Db    29 mlhgtgmksdsdqkksengvtlapedtlpflkcycsghcpddainntcitnghcfaiiee 88
         :|:::| | :   || |:| : ||     :|:| |  |||:|::|| | |:| ||::|||
Qy     2 LLRSSG-KLNVGTKK-EDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEE 59

Db    89 ddqgettlasgcmkyegsdfqckdspkaqlrrtieccrt-nlcnqylqptlppvvigpff 147
         || |   ::|||:  |||||||:|:| :: ||:|||    | ||  |:|||||:    |
Qy    60 DDSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFV 119

Db   148 dgsirwlvllismavciiamiifsscfcykhycksissrrrynrdleqdeafipvgeslk 207
         ||:|:   ||||::|| : ::::   ||| :| |   :| ||:  |||||::|| ||||:
Qy   120 DGPIHHKALLISVTVCSLLLVLIIL-FCYFRY-KRQEARPRYSIGLEQDETYIPPGESLR 177

Db   208 dlidqsqsssgsgsglpllvqrtiakqiqmvrqvgkgrygevwmgkwrgekvavkvfftte 267
         |||:|||||||||||||||||||||||:|:|||||||||||||||||||||||||||||
Qy   178 DLIEQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTE 237

Db   268 easwfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydflkcatld 327
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          ||||||||||||||||||||||||||||||||||||||||||||||||||:|| :|||
Qy    238 EASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLD 297

Db    328 trallklaysaacglchlhteiygtqgkpaiahrdlksknilikkngscciadlglavkf 387
          ::::||||||:  |||||||||::|||||||||||||||||:||||:||||||||||||
Qy    298 AKSMLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKF 357

Db    388 nsdtnevdvplntrvgtkrymapevldeslnknhfqpyimadiysfgliiwemarrcitg 447
          |||||||:| |||||||||:|||||||:||||:|||||:||||||:||:||||::|
Qy    358 ISDTNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSG 417

Db    448 giveeyqlpyynmvpsdpsyedmrevvcvkrlrpivsnrwnsdeclravlklmsecwahn 507
          |||||||||| ::|||||||||||:||:|:|||  :|||:|||||| : |||:||||:|
Qy    418 GIVEEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQN 477

Db    508 pasrltalrvkktlakmvesqdvki 532
          |||||||||:|||||| ||||:|:
Qy    478 PASRLTALRVKKTLAKMSESQDIKL 502


MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:          Tue Jun 24 17:55:41 1997;  MasPar time 18.27 Seconds
                                            783.459 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-436-265-18
Description:     (1-502) from US08436265.pep
Perfect Score:   3740
Sequence:        1 MLERSGKLNVGTKKEDGES.....TALRVKKTLAKMSESQDIKL 502

Scoring table:   BLOSUM50
                 Gap 11

Searched:        89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        pir50
                   1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
                   8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
                   13:unann9 14:unann10 15:unenc 16:unrev

Statistics:      Mean 48.874;  Variance 115.786;  scale 0.422

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES

Result          %
   No.  Score  Query Match Length DB  ID          Description            Pred. No.
 ---------------------------------------------------------------------------------
     1   3740  100.0     502 14  A53444      activin receptor-lik  0.00e+00
     2   3711   99.2     502 14  JC2491      serine/threonine kin  0.00e+00
     3   3466   92.7     502 13  A56683      receptor protein kin  0.00e+00
     4   2757   73.7     532 13  I37163      ALK-3 - human         0.00e+00
     5   2757   73.7     532 13  S37183      ALK-3 protein - huma  0.00e+00
     6   2756   73.7     532 14  JC2387      bone morphogenetic p  0.00e+00
     7   2756   73.7     532 14  A56238      bone morphogenetic p  0.00e+00
     8   2645   70.7     527 12  A54985      BMP receptor precurs  0.00e+00
     9   2505   67.0     500 14  B56238      bone morphogenetic p  0.00e+00
    10   1831   49.0     503 14  JC2061      transforming growth   1.25e-292

                                ALIGNMENTS

RESULT    1
ENTRY             A53444     #type complete
TITLE             activin receptor-like kinase 6 precursor - mouse
ORGANISM          #formal_name Mus musculus #common_name house mouse
DATE              19-May-1994 #sequence_revision 19-May-1994 #text_change
                    08-Dec-1995
ACCESSIONS        A53444; S40159
REFERENCE         A53444
   #authors       ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho,
                    M.; Miyazono, K.; Heldin, C.H.
   #journal       Science (1994) 264:101-104
   #title         Characterization of type I receptors for transforming growth
                    factor-beta and activin.
   #accession     A53444
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-502 ##label TEN
      ##cross-references GB:Z23143
REFERENCE         S40158
   #authors       Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.;
                    ten Dijke, P.
   #submission    submitted to the EMBL Data Library, June 1993
   #description   ALK-3 and ALK-6: the closely related members in the
                    serine/threonine kinase receptor family.
   #accession     S40159
      ##status         preliminary
      ##molecule_type mRNA
      ##residues       1-502 ##label MIY
      ##cross-references EMBL:Z23143
CLASSIFICATION    #superfamily protein kinase homology
FEATURE
   202-498             #domain protein kinase homology #label KIN
SUMMARY           #length 502  #molecular-weight 56944  #checksum 5099

  Query Match           100.0%;  Score 3740;  DB 14;  Length 502;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   502;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;


RESULT    2
ENTRY             JC2491     #type complete
TITLE             serine/threonine kinase receptor - rat
ORGANISM          #formal_name Rattus norvegicus #common_name Norway rat
DATE              22-Apr-1995 #sequence_revision 26-May-1995 #text_change
                    05-Jan-1996
ACCESSIONS        JC2491
REFERENCE         JC2491
   #authors       Yamaji, N.; Celeste, A.J.; Thies, R.S.; Song, J.J.; Bernier,
                    S.M.; Goltzman, D.; Lyons, K.M.; Nove, J.; Rosen, V.;
                    Wozney, J.M.
   #journal       Biochem. Biophys. Res. Commun. (1994) 205:1944-1951
   #title         A mammalian serine/threonine kinase receptor specifically
                    binds BMP-2 and BMP-4.
   #accession     JC2491
      ##molecule_type mRNA
      ##residues       1-502 ##label YAM
CLASSIFICATION    #superfamily protein kinase homology
KEYWORDS          glycoprotein; transmembrane protein
FEATURE
   127-148             #domain transmembrane #status predicted #label TMM\
   202-498             #domain protein kinase homology #label KIN\
   210-218             #region protein kinase ATP-binding motif\
   284,343,388         #binding_site carbohydrate (Asn) (covalent) #status
                         predicted
SUMMARY           #length 502  #molecular-weight 56870  #checksum 5258

  Query Match           99.2%;  Score 3711;  DB 14;  Length 502;
  Best Local Similarity 99.0%;  Pred. No. 0.00e+00;
  Matches   497;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;


RESULT    3
ENTRY             A56683     #type complete
TITLE             receptor protein kinase RPK-1 precursor - chicken
ORGANISM          #formal_name Gallus gallus #common_name chicken
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```
DATE            08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
                  08-Dec-1995
ACCESSIONS      A56683
REFERENCE       A56683
   #authors     Sumitomo, S.; Saito, T.; Nohno, T.
   #journal     DNA Seq. (1993) 3:297-302
   #title       A new receptor protein kinase from chick embryo related to
                  type II receptor for TGF-beta.
   #accession   A56683
      ##status       preliminary
      ##molecule_type mRNA
      ##residues     1-502 ##label SUM
      ##cross-references GB:D13432
CLASSIFICATION  #superfamily protein kinase homology
KEYWORDS        phosphotransferase; transmembrane protein
FEATURE
   202-498           #domain protein kinase homology #label KIN
SUMMARY         #length 502  #molecular-weight 56766  #checksum 5555

  Query Match           92.7%;  Score 3466;  DB 13;  Length 502;
  Best Local Similarity 91.6%;  Pred. No. 0.00e+00;
  Matches   460;  Conservative   23;  Mismatches  19;  Indels   0;  Gaps   0;

Db      1 mpllsssklsmesrkedsegtapappqkklscqchhhcpedsvnstcstdgycftiieed 60
          |  | ||:||:: ::|||:|:|||:|  | | | ||||||||||: ||||||||:|||| 
Qy      1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db     61 dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlhptlpplknrdfae 120
          |||  :|| |||||||||||||||||||||||||| :: ||| |||||||||:||| : 
Qy     61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db    121 gnihhkallisvtvcsillvliiifcyfrykrqearprysigleqdetyippgeslkdli 180
          | |||||||||||||:||||||:|||||||||||||||||||||||||||||||:||| 
Qy    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db    181 eqsqssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas 240
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Qy    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db    241 wfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldtkg 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|: 
Qy    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db    301 mlklayssvsglchlhtgifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| 
Qy    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db    361 tnevdippntrvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiv 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Qy    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db    421 eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas 480
          |||||||||||||||||||||||:|:|||||||||||||||||||| ||||:|||| 
Qy    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db    481 rltalrvkktlakmsesqdikl 502
          ||||||||||||||||||||||
Qy    481 RLTALRVKKTLAKMSESQDIKL 502


RESULT    4
ENTRY           I37163     #type complete
TITLE           ALK-3 - human
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
                  12-Aug-1996
ACCESSIONS      I37163
REFERENCE       I37161
   #authors     ten Dijke, P.; Ichijo, H.; Franzen, P.; Schulz, P.; Saras,
                  J.; Toyoshima, H.; Heldin, C.H.; Miyazono, K.
   #journal     Oncogene (1993) 8:2879-2887
   #title       Activin receptor-like kinases: a novel subclass of
                  cell-surface receptors with predicted serine/threonine
                  kinase activity.
   #cross-references MUID:93390967
   #accession   I37163
      ##status       preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type mRNA
      ##residues     1-532 ##label RES
      ##cross-references EMBL:Z22535; NID:g402186; CDS_PID:g402187
SUMMARY         #length 532  #molecular-weight 60201  #checksum 6778

  Query Match           73.7%;  Score 2757;  DB 13;  Length 532;
  Best Local Similarity 71.9%;  Pred. No. 0.00e+00;
  Matches   363;  Conservative   76;  Mismatches  61;  Indels   5;  Gaps   5;

Db     29 mlhgtgqksdsdqkksengvtlapedtlpflkcycsghcpddainntcitnghcfaiiee 88
          :|:::| | :   || |:| : ||     :|:| |  |||:|::|| | |:| ||::||| 
Qy      2 LLRSSG-KLNVGTKK-EDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEE 59

Db     89 ddqgettlasgcmkyegsdfqckdspkaqlrrtieccrt-nlcnqylqptlppvvigpff 147
          || |   ::|||:  |||||||:|:| :: ||:||||   | ||  |:|||||:    | 
Qy     60 DDSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFV 119

Db    148 dgsirwlvllismavciiamiifsscfcykhycksissrrrynrdleqdeafipvgeslk 207
          ||:|:   ||||::|| : ::::   ||| :| |   :| ||:  ||||::|| ||||: 
Qy    120 DGSIHHKALLISVTVCSLLLVLIIL-FCYFRY-KRQEARPRYSIGLEQDETYIPPGESLR 177

Db    208 dlidqsqssgsgsglpllvqrtiakqiqmvrqvgkgrygevwmgkwrgekvavkvfftte 267
          |||:|||||||||||||||||||||:|:|||||||||||||||||||||||||||||||| 
Qy    178 DLIEQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTE 237

Db    268 easwfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydflkcatld 327
          |||||||||||||||||||||||||||||||||||||||||||||||||||:|| :||| 
Qy    238 EASWFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLD 297

Db    328 trallklaysaacglchlhteiygtqgkpaiahrdlksknilikkngscciadlglavkf 387
          ::::|||||:  ||||||||::|||||||||||||||||:||||:|||||||||||| 
Qy    298 AKSMLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKF 357

Db    388 nsdtnevdvplntrvgtkrymapevldeslnknhfqpyimadiysfgliiwemarrcitg 447
           |||||||:| |||||||||:|||||||||:||||:|||||:||||:||:||||::| 
Qy    358 ISDTNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSG 417

Db    448 giveeyqlpyynmvpsdpsyedmrevvcvkrlrpivsnrwnsdeclravlklmsecwahn 507
          |||||||||| ::|||||||||||||:||:|:|||  :|||:|||||| : |||:||||:| 
Qy    418 GIVEEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQN 477

Db    508 pasrltalrikktlakmvesqdvki 532
          |||||||||:|||||| ||||:|:
Qy    478 PASRLTALRVKKTLAKMSESQDIKL 502

MPsrch_pp   protein - protein database search, using Smith-Waterman algorithm

Run on:          Tue Jun 24 17:54:36 1997;  MasPar time 12.58 Seconds
                                            846.231 Million cell updates/sec
Tabular output not generated.

Title:           >US-08-436-265-18
Description:     (1-502) from US08436265.pep
Perfect Score:   3740
Sequence:        1 MLLRSSGKLNVGTKKEDGES.....TALRVKKTLAKMSESQDIKL 502

Scoring table:   PAM 150
                 Gap 11

Searched:        59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
                 Listing first 45 summaries

Database:        swiss-prot34
```

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 50.508; Variance 87.156; scale 0.580

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3740	100.0	502	5	KIR6_MOUSE	SERINE/THREONINE-PROT	0.00e+00
2	3466	92.7	502	5	KIR6_CHICK	SERINE/THREONINE-PROT	0.00e+00
3	2757	73.7	532	5	KIR5_HUMAN	SERINE/THREONINE-PROT	0.00e+00
4	2756	73.7	532	5	KIR5_MOUSE	SERINE/THREONINE-PROT	0.00e+00
5	1842	49.3	501	5	KIR4_RAT	SERINE/THREONINE-PROT	0.00e+00
6	1793	47.9	503	5	KIR4_HUMAN	SERINE/THREONINE-PROT	0.00e+00
7	1700	45.5	505	5	KIR2_HUMAN	SERINE/THREONINE-PROT	0.00e+00
8	1696	45.3	505	5	KIR2_RAT	SERINE/THREONINE-PROT	0.00e+00
9	1679	44.9	509	5	KIR1_HUMAN	SERINE/THREONINE-PROT	0.00e+00
10	1669	44.6	509	5	KIR1_RAT	SERINE/THREONINE-PROT	0.00e+00

RESULT 1
ID KIR6_MOUSE STANDARD; PRT; 502 AA.
AC P36898;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R6 PRECURSOR (EC 2.7.1.37)
DE (SKP6) (ACTIVIN RECEPTOR-LIKE KINASE 6) (ALK-6).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94188705.
RA TEN DIJKE P., YAMASHITA H., ICHIJO H., FRANZEN P., LAIHO M.,
RA MIYAZONO K., HELDIN C.H.;
RL SCIENCE 264:101-104(1994).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
DR EMBL; Z23143; G437871; -.
DR PIR; A53444; A53444.
DR PIR; S40159; S40159.
DR HSSP; P01359; 1PCP.

RESULT 2
ID KIR6_CHICK STANDARD; PRT; 502 AA.
AC Q05438;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R6 PRECURSOR (EC 2.7.1.37)
DE (SKR6) (ACTIVIN RECEPTOR-LIKE KINASE 6) (ALK-6) (RPK-1).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94003400.
RA YAMAZAKI Y., SAITO T., NOHNO T.;
RL DNA SEQ. 3:297-302(1993).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
DR EMBL; D13432; G222863; -.
KW RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
KW TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 502 SERINE/THREONINE KINASE RECEPTOR R6.
FT DOMAIN 14 126 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 127 148 POTENTIAL.
FT DOMAIN 149 502 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 204 494 PROTEIN KINASE.
FT NP_BIND 210 218 ATP (BY SIMILARITY).
FT BINDING 231 231 ATP (BY SIMILARITY).
FT ACT_SITE 332 332 BY SIMILARITY.
FT CARBOHYD 44 44 POTENTIAL.
SQ SEQUENCE 502 AA; 56766 MW; D404D2DB CRC32;

Query Match 92.7%; Score 3466; DB 5; Length 502;
Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 460; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

```
Db      1 mpllsssklsmesrkedsegtapappqkklscqchhhcpedsvnstcstdgycftiieed 60
          | | ||:||:: ::|||:|:|||:|  | | | |||||||||||: ||||||||:||||
Qy      1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db     61 dsgghlvtkgclglegsdfqcrdtpiphqrrsiecctgqdycnkhlhptlpplknrdfae 120
          |||  :|| ||||||||||||||||||||||||| :: ||| |||||||||:||| :
Qy     61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db    121 gnihhkallisvtvcsillvliiifcyfrykrqearprysigleqdetyippgeslkdli 180
          | ||:|||||||||:|||||||||||||||||||||||||||||||||||||||||):|||
Qy    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db    181 eqsqssgsgsglpllvqrtiakqiqmvkqigkgrygevwmgkwrgekvavkvfftteeas 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db    241 wfreteiyqtvlmrhenilgfiaadikgtgswtqlylitdyhengslydylksttldtkg 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:
Qy    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db    301 mlklayssvsglchlhtgifstqgkpaiahrdlksknilvkkngtcciadlglavkfisd 360
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Qy    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db    361 tnevdippntrvgtkrymppevldeslnrnhfqsyimadmysfglilweiarrcvsggiv 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db    421 eeyqlpyhdlvpsdpsyedmreivcikrlrpsfpnrwssdeclrqmgklmmecwahnpas 480
          |||||||||||||||||||||||||:|:|||||||||||||||||||| ||||:||||
Qy    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db    481 rltalrvkktlakmsesqdikl 502
          |||||||||||||||||||||||
Qy    481 RLTALRVKKTLAKMSESQDIKL 502
```

RESULT 3
ID KIR5_HUMAN STANDARD; PRT; 532 AA.
AC P36894;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (EC 2.7.1.37)
DE (SKR5) (ACTIVIN RECEPTOR-LIKE KINASE 3) (ALK-3).
GN ACVRLK3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 93390967.
RA TEN DIJKE P., ICHIJO H., FRANZEN P., SCHULZ P., SARAS J.,
RA TOYOSHIMA H., HELDIN C.H., MIYAZONO K.;

RL ONCOGENE 8:2879-2887(1993).
Query Match 73.7%; Score 2757; DB 5; Length 532;
Best Local Similarity 71.9%; Pred. No. 0.00e+00;
Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 14:34:54 1997; MasPar time 4.68 Seconds
353.311 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-18
Description: (1-502) from US08436265.pep
Perfect Score: 3740
Sequence: 1 MLLRSSGKLNVGTKKEDGES.....TALRVKKTLAKMSESQDIKL 502

Scoring table: PAM 150
Gap 11

Searched: 35845 seqs, 3290575 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-[illegible]
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 33.828; Variance 163.878; scale 0.206

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	3740	100.0	502	11	PCT-US95-0	Sequence 8, Applicatio	0.00e+00
2	3711	99.2	502	10	PCT-US94-1	Sequence 4, Applicatio	0.00e+00
3	2757	73.7	532	11	PCT-US95-0	Sequence 6, Applicatio	1.10e-229
4	2756	73.7	532	10	PCT-US94-1	Sequence 2, Applicatio	1.34e-229
5	1842	49.3	501	5	US-08-317-	Sequence 17, Applicati	1.05e-148
6	1842	49.3	501	5	US-08-149-	Sequence 17, Applicati	1.05e-148
7	1831	49.0	503	10	PCT-US94-1	Sequence 10, Applicati	9.82e-148
8	1690	45.2	505	10	PCT-US94-1	Sequence 8, Applicatio	2.66e-135
9	1679	44.9	509	11	PCT-US95-0	Sequence 4, Applicatio	2.48e-134
10	1670	44.7	501	5	US-08-149-	Sequence 15, Applicati	1.54e-133

ALIGNMENTS

RESULT 1
ID PCT-US95-05467-8 STANDARD; PRT; 502 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 8, Application PC/TUS9505467.
XX
CC Sequence 8, Application PC/TUS9505467
CC GENERAL INFORMATION:
CC APPLICANT:
CC APPLICANT:
CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR

RESULT 2
ID PCT-US94-10080-4 STANDARD; PRT; 502 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 4, Application PC/TUS9410080.
XX
CC Sequence 4, Application PC/TUS9410080
CC GENERAL INFORMATION:
CC APPLICANT: GENETICS INSTITUTE, INC.
CC TITLE OF INVENTION: RECEPTOR PROTEINS
CC NUMBER OF SEQUENCES: 19
Query Match 99.2%; Score 3711; DB 10; Length 502;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 497; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Db      1 MLLRSSGKLNVGTKKEDGESTAPTARPKVLRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60
          ||||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||||
Qy      1 MLLRSSGKLNVGTKKEDGESTAPTPRPKILRCKCHHHCPEDSVNNICSTDGYCFTMIEED 60

Db     61 DSGTPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 DSGMPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFVD 120

Db    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 GPIHHKALLISVTVCSLLLVLIILFCYFRYKRQEARPRYSIGLEQDETYIPPGESLRDLI 180

Db    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 EQSQSSGSGSGLPLLVQRTIAKQIQMVKQIGKGRYGEVWMGKWRGEKVAVKVFFTTEEAS 240

Db    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 WFRETEIYQTVLMRHENILGFIAADIKGTGSWTQLYLITDYHENGSLYDYLKSTTLDAKS 300

Db    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 MLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVKFISD 360

Db    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRTHFQSYIMADMYSFGLILWEIARRCVSGGIV 420
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Qy    361 TNEVDIPPNTRVGTKRYMPPEVLDESLNRNHFQSYIMADMYSFGLILWEIARRCVSGGIV 420

Db    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAHNPAS 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||||
Qy    421 EEYQLPYHDLVPSDPSYEDMREIVCMKKLRPSFPNRWSSDECLRQMGKLMTECWAQNPAS 480

Db    481 RLTALRVKKTLAKMSESQDIKL 502
          ||||||||||||||||||||||
Qy    481 RLTALRVKKTLAKMSESQDIKL 502
```